Learning Phenotype Mapping for Integrating Large Genetic Data

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Abstract

Accurate phenotype mapping will play an important role in facilitating Phenome-Wide Association Studies (PheWAS), and potentially in other phenomics based studies. The PheWAS approach investigates the association between genetic variation and an extensive range of phenotypes in a high-throughput manner to better understand the impact of genetic variations on multiple phenotypes. Herein we define the phenotype mapping problem posed by PheWAS analyses, discuss the challenges, and present a machine-learning solution. Our key ideas include the use of weighted Jaccard features and term augmentation by dictionary lookup. When compared to string similarity metric-based features, our approach improves the F-score from 0.59 to 0.73. With augmentation we show further improvement in F-score to 0.89. For terms not covered by the dictionary, we use transitive closure inference and reach an F-score of 0.91, close to a level sufficient for practical use. We also show that our model generalizes well to phenotypes not used in our training dataset.

1 Introduction

There is a wealth of biomedical data available in public and private repositories (*e.g.* the database issue of *Nucleic Acids Research* (2011).) Along with this explosion of information comes the need to integrate data from multiple sources to achieve sufficient statistical power for analyses and/or to characterize phenomena more precisely. This trend manifests itself in two primary ways: the formation of large multi-institution multi-study consortia and public repositories. Although this situation occurs across many areas of biomedicine and our techniques are general, in this paper we will illustrate the ideas with examples from genetic studies in which we are participating.

Consider the National Center for Biotechnology Information (NCBI) database of Genotypes and Phenotypes (dbGaP) (`www.ncbi.nlm.nih.gov/gap`), that was developed to archive and distribute the results of studies that have investigated the interaction of genotype and phenotype. This is a large repository that includes genome-wide association studies (GWAS), medical sequencing, molecular diagnostic assays, as well as association between genotype and non-clinical traits. Genetic studies funded by the National Institutes of Health (NIH) over a certain size are required to submit the genetic and phenotypic data to dbGaP. There are over 130 top-level studies, 1900 datasets, 5600 analyses, comprising about 125000 phenotypic variables. Unfortunately, each study uses its own set of variables, thus far dbGaP does not attempt to reconcile, match or harmonize any of these variables. For example, a variable called `'BMI'` in one study and `'Body Mass Index'` in another study are recorded as different variables. The task of matching or harmonizing these variables falls on each researcher that obtains dbGaP data from multiple studies.

Similarly, consider a large consortium, such as the Population Architecture Using Genomics and Epidemiology (PAGE) network. PAGE (`www.pagestudy.org`) is a consortium of four major studies with the goal of understanding the association of genetic variants with complex diseases and traits across a variety of populations. The studies that comprise PAGE include: the Women's Health Initiative (WHI, www.whiscience.org/); the Multiethnic Cohort (MEC, www.crch.org/multiethniccohort/, www.uscnorris.com/mecgenetics/); the CALiCo Consortium, comprised in turn of the Atherosclerosis Risk In Communities (ARIC) study (www.cscc.unc.edu/aric/), the Coronary Artery Risk In Young Adults (CARDIA) study (www.cardia.dopm.uab.edu), the Cardiovascular Heart Study (www.chs-nhlbi.org/), the Hispanic Community Health Study (www.cscc.unc.edu/hchs/), the Strong Heart Cohort Study, and the Strong Heart Family Study (strongheart.ouhsc.edu/); and the Epidemiologic Architecture of Genes Linked to Environment (chgr.mc.vanderbilt.edu/eagle/) study, which utilizes genotypic and phenotypic data from the National Health and Nutrition Examination Surveys (NHANES) from the Centers for Disease Control and Prevention (CDC). The studies of PAGE represent a pool of over 200,000 individuals with genotypic data collected across multiple race/ethnicities, and an extremely diverse collection of phenotypic data. Within PAGE there are numerous analyses and writing groups that focus on specific diseases. Each group selects variables relevant to their disease and harmonizes the variables across studies.

A group within PAGE is investigating a novel approach to genetic association analysis called a Phenome Wide Association Studies (PheWAS) (Denny et al., 2010). This is a different approach compared to the current paradigm of Genome Wide Association Studies (GWAS) (Hardy and Singleton, 2009; Consortium, 2007). GWAS focus on calculating the association between the variation of hundreds of thousands of genotyped single nucleotide polymorphisms (SNPs) and a single or small number of phenotypes. This approach has provided valuable information about the contribution of genetic variation to a wide range of diseases and phenotypes. A common limitation of GWAS is the investigation of a limited phenotypic domain. In contrast, PheWAS utilizes an extensive range of detailed phenotypic measurements including intermediary biomarkers, in addition to prevalent and incident status for multiple common clinical conditions, risk factors, and quantitative traits for comprehensively exploring the association between genetic variations and all PheWAS phenotypes. The investigation of a broad range of phenotypes has the potential to identify pleiotropy, novel mechanistic insights fostering hypothesis generation, and to define a more complete picture of genetic variations and their impact on human diseases.

In order to compare PheWAS results across studies within PAGE to seek replication for significant genotype/phenotype associations, an important step is matching and mapping phenotypes across studies. As the number and range of phenotypes is large across studies, manually matching phenotypes is less than ideal. Therefore, an important step in improving the feasibility of PheWAS studies is to use computational approaches to map phenotypes across studies, effectively matching related phenotypes.

Definition *Phenotype Mapping* is the task of assigning every variable from each participating study to one out of a set of categories. The categories can be defined for a given integrated study or consortium, or can be taken from pre-existing ontologies, such as PhenX (www.phenx.org).

For one example, consider the variable hypt from WHI which is described by the text 'Hypertension ever' and the variable HAE5A from the EAGLE study described by the text 'Now taking prescribed medicine for HBP'. To manually match these phenotypes, a human expert declares these two variables to be relevant to class 'hypertension'. Table 1 shows additional examples.

The phenotype mapping problem is quite challenging. First, the variable descriptions are quite short (around 10 words, often less). Second, mapping the variables to a category, such as hypertension, may require significant background knowledge (HBP stands for High Blood Pressure, also known as hypertension). Third, there are large numbers of variables, so the solution needs to scale gracefully.

In summary, in order to integrate data from public repositories, such as dbGaP, or from large consortia, such as the PAGE network, a critical task is to understand how the available phenotypes relate to each other. In this paper, we present machine-learning techniques for phenotype mapping that significantly reduce the burden on researchers when integrating data from multiple studies.

2 Related Work

From the perspective of biomedical sciences, phenotype mapping is a pre-requisite and a generalization for the task of *phenotype harmonization* (Bennett et al., 2011). In harmonization, a single variable is identified or calculated for each phenotype within each study. This can only be accomplished for a very limited set of variables. There is a need, however, to provide enough information on a much larger set of phenotype variables so that researchers can determine the *common denominator* version of a measure across studies. For example, if a researcher is interested in hypertension status as an outcome, there needs to be an assessment of how hypertension status was ascertained in each study. Different approaches include self-report, clinic-based blood pressure measurement and/or anti-hypertensive medication use. Only after this information is obtained, along with other information, such as at what visit was status assessed and whether the variable is available for the entire cohort or only a portion of it will the researcher be able to determine what to use in analysis and how to interpret the findings. The phenotype mapping task that we address in this paper enables a researcher to rapidly find all the phenotype variables that are related to a given category, which then constitutes the input to the harmonization process.

From the computer science perspective, the task of phenotype mapping can be seen as an instance of the problem of entity linkage, which appears in a variety of forms across many contexts, namely record linkage (Felligi and Sunter, 1969), object identification (Tejada et al., 2001), duplicate detection (Naumann and Herschel, 2010), and coreference (Hobbs, 1979; Ng and Cardie, 2002). That is, the problem of recognizing when multiple objects (in multiple sources) actually correspond to the same entity.

Record linkage generally consists of three phases: (1) blocking, where the number of pairs of objects is reduced, which is critical for large datasets (*e.g.*, (Hernández and Stolfo, 1998; McCallum et al., 2000; Michelson and Knoblock, 2006)), (2) field similarity, where the attributes of an object are compared (*e.g.*, (Monge and Elkan, 1996; McCallum et al., 2000; Cohen et al., 2003; Bilenko and Mooney, 2003; Minton et al., 2005), and (3) record similarity, which weights how different attributes contribute to the similarity of records as a whole (*e.g.*, (Tejada et al., 2001; Bilenko and Mooney, 2003)). Machine learning techniques are used for many of these tasks.

The task of phenotype mapping is related, but differs from previous incarnations of record linkage. In our case, the variables are the objects to be mapped. However, the only attribute of an object is a terse textual description (cf. Table 1). This makes the problem harder since, as we will see, string similarity measures are not enough, and term expansion with additional background knowledge is necessary. We do not consider blocking techniques in this paper, since the number of phenotypes is in the thousands and an exhaustive $O(n^2)$ comparison is still feasible.

In this paper, we define and present an approach to phenotype mapping with good experimental performance, but there are many opportunities for refinement by incorporating additional techniques from the record linkage literature.

3 Phenotype Mapping

For the PAGE PheWAS study, phenotypes were first manually matched, through the creation of 106 phenotype classes, in order to bring together related phenotypes across studies. The following steps were then used: First, the data from different studies were filtered independently for any significant association results with $p < 0.01$. Closely related phenotypes were then matched up between studies and assigned to phenotype classes. Finally, phenotypes from all studies, regardless of association results, were matched up to the already defined phenotype classes. In this way, a phenotype that might not have shown a significant association result for a single study, but that matched a phenotype class, would still be added to the phenotype-class list. To scale up the process it is important to develop a semi or fully automatic approach for the task.

Table 1 shows some example phenotypes and their classification. **Class** labels were assigned when we manually matched the phenotypes. The real ID of a phenotype in a **study** is given in column **ID**.

Class	Study	ID	Description
Allergy	ARIC	MHQA2A	EVER TOLD HAD HAY FEVER
Allergy	ARIC	MHQA2B	STILL HAVE HAY FEVER
Allergy	EAGLEIII	ALPBERFL	Cat - flare length (mm)
Allergy	EAGLEIII	ALPCATWL	Cat - wheal length (mm)
Allergy	EAGLEIII	ALPBERFL	Cat - flare width (mm)
Allergy	EAGLEIII	ALPCATWL	Cat - wheal width (mm)
Allergy	MEC	asthma	History of Asthma, Hayfever, Skin Allergy, Food Allergy or Any Other Allergy from Baseline Questionnaire
CigaretteSmokedPerDay	ARIC	HOM32	NUMBER OF CIGARETTES PER DAY
CigaretteSmokedPerDay	ARIC	HOM35	OVERALL NUM OF CIGARETTES PER DAY
CigaretteSmokedPerDay	CHS	AMOUNT	CIGS SMOKED/DAY
CigaretteSmokedPerDay	WHI	cigsday	Smoke or smoked, cigarettes/day
Hematocrit	ARIC	HMTA01	HEMATOCRIT
Hematocrit	EAGLEIII	HTP	Hematocrit (%)
Hematocrit	WHI	hematocr	Hematocrit (%)
Hypertension	ARIC	HYPERT04	HYPERTENTION, DEFINITION 4
Hypertension	ARIC	HOM10A	HIGH BP EVER DIAGNOSED
Hypertension	CHS	HYPER_1	CALCULATED HTN STATUS
Hypertension	CHS	HYPER_2	CALCULATED HTN STATUS
Hypertension	CHS	HYPER_3	CALCULATED HTN STATUS
Hypertension	CHS	HTNMED06	ANY HYPERTENTION MEDICATION
Hypertension	EAGLEIII	HAE2	Doctor ever told had hypertension/HBP
Hypertension	EAGLEIII	HAE5A	Now taking prescribed medicine for HBP
Hypertension	MEC	q2hibp	History of High Blood Pressure from QX2
Hypertension	MEC	hibp	History of High Blood Pressure from Baseline Questionnaire
Hypertension	WHI	hypt_f30	Hypertension ever
Hypertension	WHI	htntrt_f30	Hypertension
Smoker	ARIC	CURSMK01	CURRENT CIGARETTE SMOKER
Smoker	CHS	PRESSM	PRESENT SMOKER
Smoker	WHI	smoknow	Smoke cigarettes now

Table 1: Example phenotypes and their classification

Description will be the main clue for automatic matching. These examples were chosen to illustrate unique characteristics that we observed in the manually matched data set and the challenges of the task.

- The descriptions are in a wide variety of forms. They may be a compound term, a phrase, a sentence, or even a question, and usually contain less than 10 words, so it is difficult to apply sophisticated Natural Language Processing techniques.

- Phenotypes may be related in different ways: subsumption, overlapping, at the same layer of semantic hierarchy, *etc.*

- The granularity of the classes varies. For example, we have classes as specifically defined as Hematocrit, the ratio of the volume of red blood cells to the total volume of blood. But the class Allergy covers a wide range of allergy sources and symptoms. In Table 1, we show four phenotype variables for allergies against cats with flare and wheal sizes measured. Similar variables include those for allergies of a wide range of sources: alternaria, bermuda grass, german cockroach, mite, peanut, ragweed, rye grass, Russian thistle, and white oak. While in the same class, MEC uses a single phenotype asthma to cover just about all types of allergies. On the other hand, phenotypes about cigarette smoking are distinctively divided into two categories: cigarettes smoked per day and currently smoking. As we explained earlier, the main criterion here is to maximize the chance to detect unexpected associations, not necessarily to match the most semantically similar phenotypes. As a result, directly applying conventional clustering or topic modeling techniques in Information Retrieval may not be appropriate here.

- Some phenotypes in the same class appear nearly identical. For example, the three hematocrit phenotypes have almost identical descriptions. `HYPER_1`, `2` and `3` of the study `CHS` in the class `Hypertension` have exactly the same descriptions. For those cases, applying string similarity metrics can easily match them together. However, some phenotypes in the same class appear completely different due to the use of synonyms and abbreviations. Again in class `Hypertension`, 'hypertension,' 'HTN,' 'high blood pressure,' 'HBP,' and 'high BP' are keywords appearing in the descriptions of phenotypes. It is possible for an effective string similarity metric to recognize abbreviations like 'HTN' for 'hypertension,' but without additional information there is no way for a string similarity metric to match 'hypertension' and 'high blood pressure.'

4 Methods

We formulate the task as a problem of learning to score the degree of match of a pair of phenotypes based on their descriptions. By setting a threshold of the score for match or not, the problem reduces to a standard binary classification problem in Machine Learning.

We started by performing a pre-processing step of data cleaning to remove redundant phenotypes with no description, then pairing the resulting phenotypes for training and testing in a supervised learning framework. The data is skewed as most pairs are negative.

Studies	5	Phenotypes	733
Classes	106	Total pairs	298378
Positives	10906	Negatives	287472

Table 2: Statistics of Data

Another pre-processing step is tokenization, which was applied to the description of each phenotype before we extracted a set of features from each pairs. The tokenization step includes converting all uppercase letters to lowercase letters, removing punctuations, segmenting the text into tokens, and using Porter's stemmer (Porter, 1980) to stem tokens, removing stop words and digits. For example, `'TRANSIENT ISCHEMIC ATTACK'` will become (`transient`, `ischem`, `attack`). Note that `'ic'` was removed from `'ischemic'` by the stemming process.

The next step is feature extraction. The goal here is to represent each pair of phenotype variables by a set of feature values as the input to a machine-learning model. We considered two types of features. The first type is based on string similarity metrics. The idea is to combine the strength of a variety of string similarity metrics to measure the edit distance between the descriptions of a pair of phenotypes and use the result to determine if they match each other. We chose 16 metrics as shown in Table 3. Some of them are sophisticated and designed for challenging record linkage tasks, such as matching personal records in census data.

Levenshtein Distance	
Needleman-Wunch Distance	
Smith-Waterman Distance	
Smith-Waterman-Gotoh Distance	
Monge Elkan Distance	Q-grams Distance
Jaro Distance	Jaro Winkler
Block Distance	Soundex Distance
Matching Coefficient	Dice's Coefficient
Jaccard Similarity	Overlap Coefficient
Euclidean Distance	Cosine Similarity

Table 3: String similarity metrics

We used the Java implementation provided by SimMetrics[1] to obtain the values of these metrics given a pair of phenotype descriptions. SimMetrics also provides descriptions and references of these string similarity metrics. Each metric is treated as one feature and normalized into a real value between 0 and 1, where 1 indicates that the two strings are identical.

These string similarity metrics, however, treat all words equally but apparently some words are more important than others when we match phenotypes.

[1] `staffwww.dcs.shef.ac.uk/people/S.Chapman/simmetrics.html`

To assign different weights to different words, we designed a feature set that can be considered as *weighted Jaccard* as follows. Let t be a token or a bi-gram (i.e., pair of consecutive tokens). For each t there are two features in the feature set of the following forms:

- share-t: if t appears in the pre-processed descriptions of both variables, then its value is 1 and 0 otherwise;

- miss-t: if t appears in the pre-processed description of one variable only, then its value is 1 and 0 otherwise;

For example, suppose we have tokenized variables $V_1 = (\texttt{age}, \texttt{menopause}, \texttt{start})$, and $V_2 = (\texttt{menopause}, \texttt{start}, \texttt{when})$, then the features for this pair will be

$$\begin{array}{rl}
(\text{miss-}`\texttt{age}' & :1, \\
\text{share-}`\texttt{menopause}' & :1, \\
\text{share-}`\texttt{start}' & :1, \\
\text{miss-}`\texttt{when}' & :1, \\
\text{miss-}`\texttt{age\_menopause}' & :1, \\
\text{share-}`\texttt{menopause\_start}' & :1, \\
\text{miss-}`\texttt{start\_when}' & :1).
\end{array}$$

All other features will have value 0. In this way, each example pair of variables will be represented as a very high-dimensional feature vector of binary values. The dimensionality is proportional to the square of the number of all distinct tokens appearing in the training set.

Now we are ready to train a model by a machine-learning algorithm using the examples represented as feature vectors. The model of our choice is the maximum entropy model (MaxEnt), also known as logistic regression (Hastie et al., 2009). An advantage of this model is that efficient learning algorithms are available for training this model with high-dimensional data and the model not only classifies an example into positive or negative but also gives an estimated probability as its confidence. The basic idea of logistic regression is to search for a weight vector of the same dimension as the feature vector such that this weight vector when applied in the logit function of the probability estimation of the training examples will maximize the likelihood of the positive-negative assignment of the training examples (Hastie et al., 2009). The same model can also be derived from the principle of maximum entropy. We randomly selected half of the pairs as the training examples and the rest as the holdout set for evaluation.

We used the Merriam-Webster Medical Dictionary (2006)[2] to augment the descriptions of phenotypes. If there is an entry for a token in the dictionary, then its definition will be included in the description and then the same pre-processing and feature extraction steps will be applied. Preprocessing is also required to remove useless words from the definitions in the dictionary. We chose this dictionary instead of some ontology or phenotype knowledge base for its quality of contents and comprehensive coverage of biomedical terms. The Merriam-Webster Medical Dictionary is also chosen as the only medical dictionary included in the MedlinePlus[3], a Web service produced by the National Library of Medicine for the National Institute of Health to provide reliable and up-to-date information about diseases, conditions and wellness issues to the patients and their families and friends.

5 Results

Table 4 shows the results in terms of precision, recall, and F-score. The first two rows show the use of string similarity metrics as features to train a Naive Bayes model and a MaxEnt model. The F-scores of both models are similar, but Naive Bayes has higher false positives while MaxEnt made more false negative errors. MaxEnt with weighted Jaccard outperforms one with string-similarity features. Augmentation by dictionary lookup ("w/ dictionary") is proved effective by improving recall from 0.59 to 0.82, as more positive mappings were identified for those phenotype pairs described in different terms. One may suspect that the augmentation may increase false positives due to incorrectly associating common words in the descriptions. But remarkably, the false positives also decreased, resulting in the improvement in precision as well.

Table 5 shows a set of selected examples to illustrate the effectiveness of augmentation by dictio-

[2] www.m-w.com/browse/medical/a.htm

[3] www.nlm.nih.gov/medlineplus

Method / Model	Precision	Recall	F-score
String similarity metrics feature			
NaiveBayes	0.5236	0.6492	0.5797
MaxEnt	0.8092	0.4760	0.5994
Weighted Jaccard			
MaxEnt	0.9655	0.5931	0.7348
w/ dictionary	0.9776	0.8208	0.8924
w/ transitive closure (depth= 1)	0.9138	0.8064	0.8568
w/ both	0.8961	0.9177	0.9068

Table 4: Performance results

Phenotypes	w/o dic	Score	w/ dic	Score
Goiter ever Overactive thyroid ever	0	0.014562	1	0.996656
History of High Blood Pressure from Baseline Questionnaire Hypertension ever	0	0.014562	1	0.641408
DIABETES W/ FASTING GLUCOSE CUTPT.<126 Insulin shots now	0	0.014562	1	0.523262
TIA STATUS AT BASELINE Stroke	0	0.014562	1	0.517444
NUMBER OF CIGARETTES PER DAY CIGS SMOKED/DAY	0	0.014562	0	0.002509

Table 5: Examples of Mapping Results

nary lookup. The first column shows the original descriptions of the phenotype variable pairs. The second and third columns show the classification results (0 for negative, 1 for positive) and the confidence scores by the MaxEnt model without augmentation. The next two columns are their counterparts for the model with augmentation.

For example, the definition of ‘Goiter’ is ‘an enlargement of the thyroid gland.’ Therefore, after augmented by dictionary lookup, goiter can be matched with overactive thyroid. Similarly, it is now possible to match ‘High Blood Pressure’ with ‘hypertension’ and ‘TIA’ with ‘stroke.’ ‘DIABETES’, ‘GLUCOSE’ and ‘Insulin’ can also be associated together.

However, terms must be covered in the medical dictionary for this method to work. For example, since ‘CIGARETTES’ is not a medical term and even the most sophisticated string similarity metrics cannot match the local abbreviation ‘CIGS’ to ‘CIGARETTES’, both models failed to match ‘SMOKE’ and ‘CIGARETTES’ together.

A solution to this issue is to compute transitive closure of the mapping. For example, if

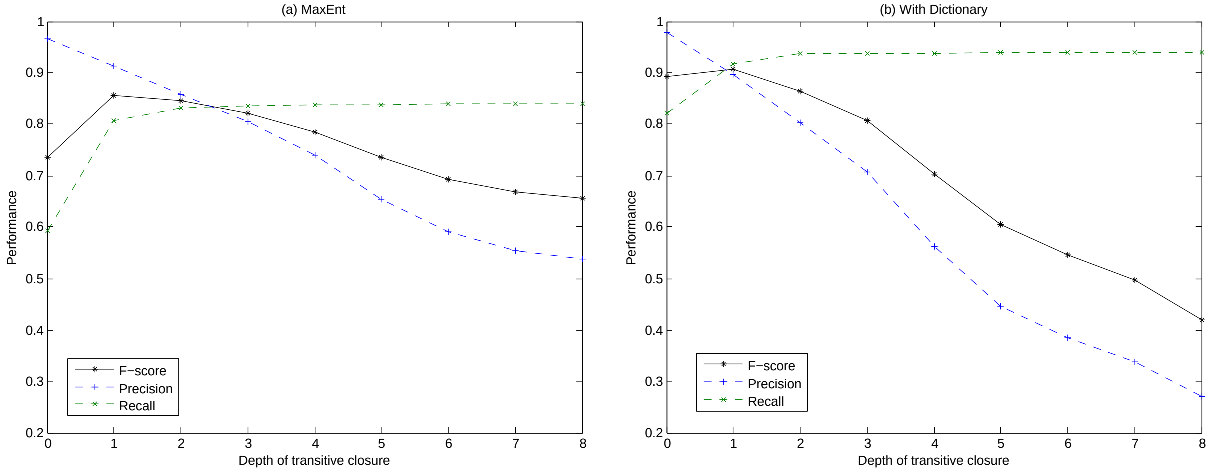
$$\begin{aligned} V_1 &= (\texttt{SMOKE}) \quad \text{and} \\ V_2 &= (\texttt{SMOKE CIGARETTES}) \end{aligned}$$

are matched together by the model because of a shared term ‘smoke’ and so are V_2 and

$$V_3 = (\texttt{cigarettes}),$$

but not V_1 and V_3, then transitive closure will infer a match of V_1 and V_3. That will improve recall and F-score further.

Figure 1 shows the performance of applying increasing depths of transitive closure to the results (a) without and (b) with augmentation by dictionary lookup. Transitive closure improves the performance for both models in the beginning but degrades quickly afterward because a phenotype may be assigned to multiple classes. As false positives increase, they will ripple when we infer new positives from false positives. Improvement for the model (a) is more obvious and degradation is not as grave. Applying transitive closure with depth $= 1$ yields the



(a) MaxEnt model

(b) MaxEnt model with augmentation by dictionary lookup

Figure 1: Performance with increasing depths of transitive closure

best performance. The exact scores are shown in Table 4 (See "w/ transitive closure" and "w/ both").

The results above were obtained by splitting the set of all pairs by half into training and test sets. It is possible that the model *remembers* phenotype descriptions because they distribute evenly in both training and test sets. To apply the system in practice, the model must generalize to unseen phenotypes. To evaluate the generalization power, instead of splitting the set of pairs, we split the set of variables by 2 to 1, and used $2/3$ of phenotype variables to generate pairs as the training set and $1/3$ to pair with those in the $2/3$ set as well as with each other for testing. That resulted in 129286 pairs for training and 169092 pairs for testing. In this test set, 6356 pairs are positive.

We used this training set to train MaxEnt models using the weighted Jaccard feature set with and without dictionary augmentation. Table 6 shows the results. Again, dictionary augmentation significantly improves the performance in this case, too, with the F-score reaching 0.81. Though the results degrade slightly from the ones obtained by splitting by pairs, this is expected as the training set is smaller (129286 pairs vs. $149189 = 298378/2$, see Table 2). Consequently, the proposed models can generalize well to unseen phenotypes to some extent.

Method/Model	Precision	Recall	F-score
w/o dictionary	0.9398	0.5817	0.7186
w/ dictionary	0.8213	0.7977	0.8093

Table 6: Performance results of splitting by variables

6 Conclusions and Future Work

In this paper, we define the problem of phenotype mapping and present a solution by learning to score and classify pairs of phenotypes. We evaluate our solution using a data set of manually matched phenotypes from the PAGE PheWAS study. We show that weighted Jaccard features are more effective for this problem than combining string similarity metrics for a MaxEnt model and that dictionary augmentation improves the performance by allowing matching of phenotypes with semantically related but syntactically different descriptions. We show that inferring more positives by depth-one transitive closure fixes those false negatives due to the lack of dictionary definitions. Finally, the evaluation results of splitting-by-variables show that the models generalize well to unseen variables, which is important for the solution to be practical.

Our future work includes to apply blocking as a pre-processing step to keep the number of pairs manageable and to apply active or unsupervised learning to alleviate the burden of generating training corpora by manual matching.

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