Structural dynamics is a determinant of the functional significance of missense variants

Luca Ponzoni* and Ivet Bahar*1

*Department of Computational and Systems Biology, School of Medicine, University of Pittsburgh, Pittsburgh, PA 15261

Edited by Robert L. Jernigan, Iowa State University, Ames, IA, and accepted by Editorial Board Member J. A. McCammon March 13, 2018 (received for review September 9, 2017)

Accurate evaluation of the effect of point mutations on protein function is essential to assessing the genesis and prognosis of many inherited diseases and cancer types. Currently, a wealth of computational tools has been developed for pathogenicity prediction. Two major types of data are used to this aim: sequence conservation/evolution and structural properties. Here, we demonstrate in a systematic way that another determinant of the functional impact of missense variants is the protein’s structural dynamics. Measurable improvement is shown in pathogenicity prediction by taking into consideration the dynamical context and implications of the mutation. Our study suggests that the class of dynamics descriptors introduced here may be used in conjunction with existing features to not only increase the prediction accuracy of the impact of variants on biological function, but also gain insight into the physical basis of the effect of missense variants.

Significance

Discrimination of clinically relevant mutations from neutral mutations is of paramount importance in precision medicine and pharmacogenomics. Our study shows that current computational predictions of pathogenicity, mostly based on analysis of sequence conservation, may be improved by considering the changes in the structural dynamics of the protein due to point mutations. We introduce and demonstrate the utility of a classifier that takes advantage of efficient evaluation of structural dynamics by elastic network models.

Author contributions: L.P. and I.B. designed research; L.P. performed research; L.P. and I.B. contributed new reagents/analytic tools; L.P. and I.B. analyzed data; and L.P. and I.B. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission. R.L.J. is a guest editor invited by the Editorial Board.

This open access article is distributed under Creative Commons Attribution-NonCommercial-NoDerivatives License 4.0 (CC BY-NC-ND).

Data deposition: The method presented in this paper has been implemented on the web server RAPSDY (Re-Assessment of Pathogenicity of SAVs based On Dynamics; rapsody.csb.pitt.edu). The integrated dataset used for training and the source code are available at rapsody.csb.pitt.edu/download.html.

1To whom correspondence should be addressed. Email: bahar@pitt.edu.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1715896115/-/DCSupplemental.
Dynamics-Derived Features and DYN/SEQ-Based Predictors. To explore whether features derived from structural dynamics, referred to as dynamical (DYN) features, can help improve the overall accuracy of variant classification, we considered the following features: (i) gaussian network model (GNM)-based mean-square fluctuations (MSF) of residues, where minima indicate the sites that potentially act as hinges for supporting the protein square fluctuations (MSF) of residues, where minima indicate the sites that potentially act as hinges for supporting the protein; and (ii) the propensity of residues to act as sensors or as effectors of allosteric signals (27) based on perturbation-response scanning (PRS) analysis (28) of their ability to sense or transmit local geometry.

The binary classification of variants into deleterious or neutral might be an oversimplification, being inadequate for capturing the variance spectrum of effects inducible by a mutation [see, for instance, the distinction between “rhoeostat” and “toggles” in an earlier study (15)]. However, our aim is to demonstrate in a quantitative way the utility of adopting new features based on structure-encoded dynamics and providing a classifier that permits the assessment of the pathogenicity of SAVs in light of protein dynamics. This type of binary measure allows us to have access to a sufficiently large source of data as input. The outputs, on the other hand, help shed light on possible structural and dynamic origins of the impact of mutations at the molecular level.

DYN features capture the global properties of the protein—that is, those originating from the overall 3D topology of inter-residue contacts. As such, they provide a metric for assessing the effect of mutation on the overall (global) dynamics, as opposed to physicochemical features such as SASA, which depend on the local geometry.

DYN features are purely position dependent: They do not depend on the identity of the amino acid at that position. To distinguish between variants that occur at the same site but involve different amino acid mutations, we used two sequence-dependent (SEQ) features extracted from PolyPhen-2 (2, 32): (i) the conservation score of the WT amino acid represented by the position-specific independent counts (PSIC) score (WT PSIC); and (ii) the difference between the PSIC scores of the WT and mutant amino acids (APSIC). The classification of SAVs into deleterious or neutral was performed using a Random Forest (RF) metaestimator, implemented in the open-source machine learning Python library Scikit-learn (33). The method is robust to overfitting and requires minimal parameter optimization (see SI Appendix, Supplementary Methods and Fig. S1 for details).

Comparative Analysis Highlights the Utility of DYN Features for Accurate Assessment of the Effect of Mutations. For assessing the importance of including protein dynamics in pathogenicity prediction, we compared the output from the DYN/SEQ-based predictors to those obtained with 11 pathogenicity prediction tools: (i) Mutation Taster-2; (ii) PolyPhen-2; (iii) Mutation Assessor; (iv) Combined Annotation Dependent Depletion; (v) SIFT; (vi) likelihood ratio test; (vii) FatHMM-U; (viii) GERP++ and (i) phyloP, which have been developed independently; and (v) Condel and (a) Logit, which are metapredictors that combine the predictions from PolyPhen-2, SIFT, and Mutation Assessor. Three of these tools (Mutation Taster-2, PolyPhen-2, and Mutation Assessor) have been partially trained on some of the benchmark datasets. Thus, their predictions, and those of the two metapredictors that utilize them, are affected by training bias (26). Each tool returns a pathogenicity score (accessible in the supplementary data of ref. 26) for each variant, which represents the expected probability of having a deleterious effect on function. In addition to these 11 predictors, we also considered three predictors—FatHMM-W, Condel+, and Logit—that have been reported to suffer from the so-called “black hole” bias (26); in these three cases, the classifier is biased toward assigning one dominant class of SAVs, deleterious or neutral, to all mutations in a given protein. These predictors benefit from the fact that many proteins in the available datasets contain almost exclusively one class of variants (either neutral or deleterious). The set of 14 tools, including these additional three, is called the extended set of predictors.

Results are presented in Fig. 1 A–E. For each dataset, shown on a separate panel, we report the results from testing our predictor based on SEQU, DYN features exclusively and on their combination (SEQ+DYN) to two sets of results: one for the RF classifiers trained/tested through cross-validation on the same dataset (red bars in Fig. 1 A–E) and the other for a classifier trained on the four other datasets (green bars). The results from the 11 predictors listed above are shown in solid blue bars in Fig. 1 A–E, and those benefiting from training bias in dashed blue bars.

SI Appendix, Fig. S2 displays the counterpart of Fig. 1 A–E for the extended set of predictors, with the results from the three additional predictors shown in gray bars. The prediction accuracy is measured by the area under the curve (AUC) evaluated for the receiver operating characteristic (ROC) curve. The AUC is 0.5 for random classification (main diagonal), and 1 for perfect classification. SI Appendix, Fig. S3 illustrates the ROC curves [i.e., true-positive (TP) rate (sensitivity) against false-positive (FP) rate (specificity)] obtained using our classifiers (SI Appendix, Fig. S3A) and the extended set of classifiers (SI Appendix, Fig. S3B) on the Integrated Dataset.

Several observations are made in Fig. 1 A–E and SI Appendix, Fig. S2. First, despite its simplicity [e.g., being trained on a reduced set of structurally known proteins (about 25% of the complete set); SI Appendix, Table S1] and the use of a small number of easily computed features, SEQ+DYN predictions exhibit accuracy levels comparable to, and in some cases better than, those obtained by the other advanced methods. The AUCs for SEQ+DYN rank always among the top when excluding the cases affected by training bias. Second, SEQ+DYN performance shows little dependency on the training procedure (red vs. green bars), whereas other methods generally show a pronounced decrease in AUC when tested against datasets other than their training datasets (compare the dashed and solid blue bars for the same method across different panels in Fig. 1 A–E). An outlier is the VariBenchSelected dataset in Fig. 1C, which will be discussed later.

Closer examination shows that the SEQ-only classifier outperforms DYN-only in the cases of the HumVar dataset (red and green bars in Fig. 1 A–E), the ExoVar dataset (red bars), and the...
specialized SwissVarSelected dataset (green bars), distinguished by a low population of deleterious SAVs. This dominant role of SEQ features is also supported by the analysis of the relative contributions (weights) of features, presented in Fig. 1F. A plausible explanation is the consideration of the specific type of amino acid substitution by SEQ features, whereas DYN features are solely based on the position of the mutated residue. On the other hand, the usefulness of SEQ features depends crucially on the quality of the MSA used for computing them, which explains why their contribution is particularly strong in the two datasets (HumVar and ExoVar) specifically designed for training PolyPhen-2. In contrast, the DYN classifier outperforms the SEQ classifier when tested against VariBenchSelected and predictSNPSelected.

As previously mentioned, VariBenchSelected exhibits a unique behavior: the AUC plot in Fig. 1C shows an unusually high accuracy in the SEQ+DYN cross-validation analysis. The disparity between the red and green bars in Fig. 1C suggests that this behavior originates from the nature of the dataset itself. A closer investigation shows that a considerable fraction of SAVs (~40%; see SI Appendix, Table S1) in this dataset are in the form of multiple mutations at the same site in a given protein—that is, there is a preponderance of variants with different types of amino acid substitutions at the same position. In addition, nearly all such same-site variants are assigned the same pathogenicity class (see SI Appendix, Table S1, column 6). This leads to a situation where the classifier is trained to assign less weight to amino acid identity and more to its position; hence, the success of DYN features (red bars in Fig. 1F), which are agnostic to amino acid identity but take account of the position in the 3D structure. This also explains the high AUC values in SEQ+DYN cross-validation.

**RF Classifier Trained on the Integrated Dataset Outperforms Existing Unbiased Predictors.** We also evaluated the level of accuracy obtained by the RF classifiers applied to the Integrated Dataset, using a 10-fold cross-validation procedure. Fig. 2A presents the results in comparison with other prediction tools. The SEQ+DYN classifier outperforms all others in this case. The accuracy (AUC) obtained by SEQ+DYN (first red bar in Fig. 2A) is 0.83, the highest among all the considered tools, except for those benefiting from type 2 bias (SI Appendix, Fig. S4A). Since same-site SAVs amount to a significant fraction in some datasets (SI Appendix, Table S1), we repeated the analysis by making sure that same-site variants were not simultaneously present in both the training and test sets. The results (orange bars in Fig. 2A), show a slight decrease in the AUC (0.79) for the SEQ+DYN classification. The method’s accuracy remains higher, however, than all other unbiased methods.

It is interesting to note in Fig. 2A that the DYN-based classifier slightly outperformed the SEQ-based classifier; this may be attributed to limitations in MSA quality and the inclusion of only two SEQ features, as opposed to six DYN features. Indeed, the individual SEQ features make larger contributions to decision making (Fig. 2B, tan bars) than individual DYN features. Exclusion of same-site SAVs had a minimal effect on the contribution of features (Fig. 2B, blue bars). Fig. 2C depicts in a more comprehensible manner the discriminatory power of the three classifiers, displaying the histograms of predictions (scores) collected during cross-validation. The SEQ+DYN histogram is used to evaluate pathogenicity probabilities (SI Appendix, Fig. S5).

We further compared the performance of the different tools using an expanded list of metrics, listed in SI Appendix, Table S2. Since the class imbalance might skew a few specific metrics, like the AUC of the precision-recall curve (SI Appendix, Fig. S6), we also provide as a reference the comparison with random classifications, artificially biased toward either deleterious or neutral classes. Results in SI Appendix, Table S3 show that the SEQ+DYN
classifier ranks among the top performers across all metrics, even when considering those quantities centered on predictions of neutrals (e.g., specificity = TN/(FP+TN) and negative predictive value = TN/(TN+FN), where TN is true negative and FN is false negative).

Additional comparison reveals the decrease in the performance of the three tools benefiting from type 2 bias when datasets of proteins with more balanced distributions of deleterious and neutral mutations are used as benchmark. **SI Appendix, Fig. S4B** displays the results for the complete set of “mixed” proteins, which have both neutral and deleterious mutations. The performances of our RF classifiers and the 11 prediction tools are only moderately lowered, if any, compared with those observed for the original (Integrated) dataset, whereas there is a drop in the AUC values of the three tools (gray bars in **SI Appendix, Fig. S4B**) that no longer benefit from type 2 bias. This effect is further pronounced when considering increasingly smaller subsets of proteins, with the deleterious-to-neutral ratio progressively approaching 1 (**SI Appendix, Fig. S7**). These results demonstrate that our classifiers are robust against the changes in the dataset composition.

**Examination of Significance of DYN Features Reveals the Competing Roles of Allosteric Signaling Sites.** Our analysis provides insight into the role of structural dynamics in general, and individual dynamic features in particular, in shaping the effect of missense variants. Fig. 3 provides a visual assessment of the ability of each of the SEQ and DYN features to discriminate between deleterious and neutral SAVs. In each case, we display two histograms, representing the distributions of deleterious (shown in red) and neutral (shown in blue) mutations. Sharper differences indicate higher discrimination power of the feature.

![Fig. 3. Histograms of SEQ and DYN features for neutral and deleterious variants. Each panel refers to a distinctive feature (see absissa). The two histograms refer to the subgroups of deleterious (shown in red) and neutral (shown in blue) mutations. Sharper differences indicate higher discrimination power of the feature.](Image)

The DYN-based classifier can detect a new class of deleterious sites while assisting in improving pathogenicity predictions.

**Fig. 4.** Comparative analysis of prediction accuracy of DYN- and/or SEQ-based RF classifiers and PolyPhen-2 applied to 20 mixed proteins. The proteins (listed in **SI Appendix, Table S4**) are organized along the absissa in the order of decreasing AUC obtained by the SEQ+DYN classifier.

![Fig. 4.](Image)
ID code 5do7, chain B), which yields a lower AUC using the SEQ+DYN classifier compared with that obtained by SEQ-only. In both cases, the biological assembly comprises multiple chains. Reevaluation of DYN features by considering the intact structures of the assemblies instead of the single chains leads to improved AUC values (SI Appendix, Fig. S8). This analysis highlights the importance of considering the biological assembly for improved evaluation of DYN features.

In Fig. 5 and SI Appendix, Fig. S9, we examine more closely two other cases. The confusion matrices in Fig. 5 A–C and SI Appendix, Fig. S9 A–C display the predicted pathogenicity score as a function of residue index, organized in two classes: neutral and deleterious residues. Each class is further divided into two subgroups, depending on predicted pathogenicity scores: TPs and FNs (for deleterious sites) and FPs and TNs (for neutral sites). The threshold scores that separate these subgroups are optimized to maximize the differentiation between the subgroups. A “perfect” classifier would populate the TP block (Fig. 5 A–C and SI Appendix, Fig. S9 A–C. Upper Right, red dots) and TN block (Lower Left, blue dots) of the confusion matrix, and exclude the FP block (Upper Left, cyan x’s) and FN block (Lower Right, orange x’s). It is interesting to note that among SEQ+DYN misclassifications, FNs are much more common than FPs—that is, the classifier misses a few deleterious SAVs, while it correctly predicts almost all neutral SAVs.

For a closer examination of the outcomes, we generated color-coded diagrams (Fig. 5 D–F and SI Appendix, Fig. S9 D–F) that enable the comparative visualization of the accurate predictions (TP shown in red and TN shown in blue) and inaccurate predictions (FP shown in cyan and FN shown in orange). Deleterious SAVs (red and orange) are usually located in the protein’s interior, and those incorrectly predicted to be neutral (orange) are usually on the surface, signaling that more discriminative classifiers are needed to detect those deleterious sites. We note in this respect that the DYN classifier assists in such cases. An example is M133 in the hydrolase illustrated in Fig. 5. The latter is misclassified as neutral by SEQ-based predictor because M133 is not evolutionarily conserved. On the other hand, it is correctly recognized to be potentially deleterious, if mutated, by the DYN classifier, as it satisfies many DYN criteria: high propensity to act as effector, low propensity to act as a sensor, low conformational flexibility (probed by SASA and MSF), and high stiffness and mechanical bridging ability (Fig. 5G); and the DYN features dominate the outcome in the DYN+SEQ classifier. SI Appendix, Fig. S9 illustrates a case where a mutation (R589H in an anion transport protein) inaccurately assessed to be neutral by either the SEQ or DYN classifier is correctly predicted to be deleterious using SEQ+DYN. These examples suggest that the SEQ+DYN classifier can synergistically predict the actual effects of the missense variants when SEQ and/or DYN classifiers fail to do so.

A Test Case: CFTR Variants. A recent study of cystic fibrosis transmembrane conductance regulator (CFTR) variants (34) presents a list of variants organized into three categories: (i) those commonly associated with cystic fibrosis (CF); (ii) those associated with a bicanonical defect in channel function, leading to disorders like pancreatitis but not cystic fibrosis (BD); and (iii) those reported in previous chronic pancreatitis genetic studies, but without strong evidence of pathogenicity (“others”); see SI Appendix, Fig. S10A. Results from our evaluation of these variants are presented in SI Appendix, Table S5 and Fig. S10B. The most striking observation is that 9 of 13 “other” variants are classified as neutral, in contrast to most of the assignments listed in the Integrated Dataset (SI Appendix, Table S5, column 11) and most of the predictions from PolyPhen-2. Moreover, 6 of 10 CF/BD variants are classified as deleterious, in line with the results of the pancreatitis study (34). It is remarkable that most of deleterious variants predicted by our classifier fall in the CF/BD categories. The remaining variants, whose functional impact is still debated, mostly predicted to be neutral, will need future studies for possible verification.

Fig. 5. Illustration of detailed analysis for human α-L-iduronidase (PDB ID code 3w81, chain A). (A–C) Confusion matrices for the three RF classifiers—that is, the predicted pathogenicity score for the two subgroups of variants, ordered by residue index along the abscissa. Lower Left and Upper Right submatrices represent the accurately predicted neutral variants (TN, blue dots) and deleterious variants (TP, red dots). The off-diagonal entries are the FPs (cyan x’s) and FNs (orange x’s). The threshold value (horizontal dashed line) for pathogenicity is chosen according to the Youden’s index (39) (SI Appendix, Supplementary Methods). (D–F) Corresponding ribbon diagrams, where mutation sites (spheres) are color-coded by the dots in the confusion plots (i.e., blue or red refers to correctly predicted neutral or deleterious residues, respectively). A number of FNs (shown in orange) in E occur on the surface of the protein, where amino acid-specific features presumably weigh more than structural/dynamical ones in defining functionality (e.g., recognition). The prediction for variant R105Q, on the other hand, estimated to be an FP (shown in cyan) based on sequence only, is now corrected upon inclusion of DYN features. (G) DYN feature profiles as a function of residue index. The dashed vertical line indicates the position of M133, recognized as a TP by the DYN classifier and misclassified by the SEQ classifier. The asterisks indicate those features for which low values give rise to deleterious mutations.
Conclusion

With the steady increase in genome-scale data made available in recent years, it has become essential to develop tools that can extract useful information in a systematic, efficient, and robust way. In this study, we built on past research in the field of pathogenicity prediction of SAVs, as well as recent advances in genome-scale characterization of protein dynamics (35), to test and demonstrate the validity of our hypothesis: that structural dynamics, not only sequence or structure, might be considered a determinant of the effect of missense variants on biological function. Our analysis showed that a measurable improvement is achieved when DYN and SEQ features are combined.

Our study also provided insight into the interpretation of the functional impact of variants in the light of the intrinsic dynamics of the mutated site. We could confirm the current understanding of functional impact prediction wih regard to the localization of dynamically important residue positions that are more likely to incur detrimental mutations. In the specific case of the sensitivity measurements obtained from PRS analysis, however, we produced evidence in support of the concept that residues identified as important residue positions that are more likely to incur detrimental mutations. In the specific case of the sensitivity measurements, however, we produced evidence in support of the concept that residues identified as important residue positions that are more likely to incur detrimental mutations.

Lastly, we focused on a few case studies that highlighted the tendency of deleterious mutations to localize in the core of a protein. A corollary would be that variants at exposed regions would be neutral, but this is not the case. The frequent occurrence of FNs at those regions indicates that accurate prediction of (dys)functional regions remains a challenge. This is mainly due to a competition between adaptability to promiscuous interactions (which are functional in a given organism/pathway and need to be retained) and the inherent conformational malleability (which can tolerate substitutions without affecting other regions). The combination of DYN- and SEQ-based features emerges as a useful tool for improving the accuracy of predictions at such challenging sites.

Materials and Methods

SAV datasets for training and testing of the RF classifiers and evaluating pathogenicity scores and labels for the 14 prediction tools were extracted from previous work (26) and summarized in Si Appendix, Table S1. The variants used in this work are those SAVs for which an associated PDB structure exists. We mapped between SAV sequences and PDB structures using the UniProt database (36). GNM- and ANM-predicted DYN properties were calculated using the ProDy application programming interface (22). MBS (29) was computed with code adapted from ref. 37, and SASAs were computed using the DSSP program (31). The SEQ features based on the PSIC score (38) were extracted from PolyPhen-2 (2, 32).

The details on the DYN/SEQ features and the RF algorithm are presented in Si Appendix, Supplementary Methods. The method presented in this paper has been implemented on the server RAPSODY (Re-Assessment of Pathogenicity of SAVs based On Dynamics; rapsody.csb.pitt.edu). The integrated dataset used for training and the source code are available at rapsody.csb.pitt.edu/download.html.

Acknowledgments

We acknowledge useful discussions with Dr. David Whitcomb on CFTR variants and with Dr. Sean Mooney on PolyPhen-2. Support from NIH Grants P41 GM103712 and U54 HG008540 (to I.B.) is gratefully acknowledged.