

Structural bioinformatics

A comprehensive assessment of long intrinsic protein disorder from the DisProt database

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Abstract

Motivation: Intrinsic disorder (ID), i.e. the lack of a unique folded conformation at physiological conditions, is a common feature for many proteins, which requires specialized biochemical experiments that are not high-throughput. Missing X-ray residues from the PDB have been widely used as a proxy for ID when developing computational methods. This may lead to a systematic bias, where predictors deviate from biologically relevant ID. Large benchmarking sets on experimentally validated ID are scarce. Recently, the DisProt database has been renewed and expanded to include manually curated ID annotations for several hundred new proteins. This provides a large benchmark set which has not yet been used for training ID predictors.

Results: Here, we describe the first systematic benchmarking of ID predictors on the new DisProt dataset. In contrast to previous assessments based on missing X-ray data, this dataset contains mostly long ID regions and a significant amount of fully ID proteins. The benchmarking shows that ID predictors work quite well on the new dataset, especially for long ID segments. However, a large fraction of ID still goes virtually undetected and the ranking of methods is different than for PDB data. In particular, many predictors appear to confound ID and regions outside X-ray structures. This suggests that the ID prediction methods capture different flavors of disorder and can benefit from highly accurate curated examples.

Availability and implementation: The raw data used for the evaluation are available from URL: <http://www.disprot.org/assessment/>.

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Supplementary information: [Supplementary data](#) are available at *Bioinformatics* online.

1 Introduction

For almost a century, our view on protein function has been dominated by the structure-function paradigm, which assumed that for functioning, a protein needs to fold into a stable three-dimensional (3D) structure. Due to its exquisite explanatory power, this

paradigm became practically exclusive, fueling efforts to solve structures of proteins and other macromolecules on an almost industrial scale. As a result, more than 100 000 high-resolution structures have been deposited into the Protein Data Bank (PDB) (Velankar *et al.*, 2016). Recently, however, it has been recognized that many

proteins, or regions of proteins, lack such stable 3D structures under apparently native conditions, which challenged the structure-function paradigm. These intrinsically disordered (ID) proteins or regions are prevalent in most organisms (Peng *et al.*, 2015; Xue *et al.*, 2012). They fulfil important functions in the cell, mostly related to cellular signaling and molecular recognition (Habchi *et al.*, 2014; van der Lee *et al.*, 2014; Oldfield and Dunker, 2014), when they often undergo induced folding in the presence of their partner (Tompa *et al.*, 2015). The phenomenon of structural disorder is also under intense scrutiny because, due to their regulatory importance, disordered proteins are often implicated in diseases (Uversky *et al.*, 2008) and represent important drug targets (Hu *et al.*, 2016; Joshi and Vendruscolo, 2015; Metallo, 2010).

Whereas contrasting ID proteins or regions with folded proteins might seem to provide a clear definition, there is actually no consensus in the field with regards of what should be considered as structural disorder. As a rudimentary definition, the lack of a stable 3D fold might work, but it does not unequivocally translate to experimental or computational approaches to identify disorder. In accord, a variety of experiment techniques, which may be considered primary (X-ray crystallography and NMR) or secondary (CD spectroscopy, limited proteolysis and many more) (Habchi *et al.*, 2014; Uversky and Dunker, 2012) provide different types of information on the lack of structure. It has been previously argued that ID should only be accepted when they all agree (Habchi *et al.*, 2014). Due to technical difficulties, this consensus is not usually pursued, and thus the entries in the recently updated version of the database of protein disorder, DisProt (Piovesan *et al.*, 2017), come in different subtypes, depending on the type of the experimental evidence that supports their annotation. In other words, structural disorder appears to come as different ‘flavors’, the relationship of which is difficult to assess at the moment. We may distinguish flavors of disorder by distinct amino acid composition (Vucetic *et al.*, 2003), backbone flexibility (Cilia *et al.*, 2013; Martin *et al.*, 2010), evolutionary conservation (Bella *et al.*, 2011), function (Peng *et al.*, 2015; Tompa, 2005; Xue *et al.*, 2012) and length. The separation of ID regions into short and long disorder usually involves a threshold of 20 or 30 continuous disordered residues. By this definition, short disorder is often present in the PDB in the form of short linkers or loops in folded proteins, whereas long disorder is underrepresented in the PDB because it poses major obstacles in structure determination. In accord, as many entries in the previous version of DisProt (Sickmeier *et al.*, 2007) have been identified as regions with missing coordinates in PDB X-ray structures, DisProt v 6.0 was dominated by short IDRs. The recent update (DisProt v 7.0) relies much more on NMR and secondary techniques, thus the length distribution is significantly shifted towards longer ID regions (Piovesan *et al.*, 2017).

This notable heterogeneity has bearings on the prediction of structural disorder from sequence. Today, dozens of bioinformatics predictors are available for assigning to amino acids in a sequence the status of order or disorder (Atkins *et al.*, 2015; He *et al.*, 2009). As predictors rely on different principles, they are sensitive to the sequence environment, biased not only by the actual protein, but also the experimental methodology used for describing its disorder. In brief, available disorder prediction methods assess structural disorder based on: i) (amino acid) propensities, ii) pseudo-energy functions of inter-residue contacts, iii) machine learning approaches and iv) consensus based approaches (Atkins *et al.*, 2015; He *et al.*, 2009). Propensity-based predictors apply some simple statistics on the physical/chemical features of amino acids, such as amino acid composition (Prilusky *et al.*, 2005), secondary structure propensity (Linding *et al.*, 2003a), or regions with high structural temperature

factors (Linding *et al.*, 2003b). Predictors based on pseudo-energy functions (contact potentials) rely on statistics of residue contacts in folded proteins to recognize sequence regions that are in a high-energy (and thus disordered) state (Dosztányi *et al.*, 2005; Galzitskaya *et al.*, 2006). Machine learning algorithms (neural networks and support-vector machines) are trained to recognize features that distinguish a collection of positive (disordered) sequences from negative (ordered) proteins (Ishida and Kinoshita, 2007; Jones and Cozzetto, 2015; Vullo *et al.*, 2006; Wang *et al.*, 2012, 2016; Walsh *et al.*, 2012; Zhang *et al.*, 2017). The results of distinct algorithms may also be combined into meta-predictors. Such consensus-seeking algorithms (Ishida and Kinoshita, 2008; Mizianty *et al.*, 2010; Necchi *et al.*, 2017; Walsh *et al.*, 2011; Xue *et al.*, 2010) are more accurate than individual predictors, but they offer no indication of the cause of disorder and may combine individual predictions that vary in disorder output and parameter setting.

In all, predictors in the first two categories approach structural disorder by physical principles, conveying an element of understanding of the reasons of structural disorder of a region. Predictors in the other two categories, on the other hand, are trained to recognize sequences that look like other disordered sequences, propagating the uncertainty of the experimental identification of structural disorder (ascertainment bias), and do not convey a physical sense of disorder. It should also be appreciated that distinct predictors have different sensitivity in capturing different flavors of disorder, and thus perform differently on different ID collections, as demonstrated in the Critical Assessment of techniques for protein Structure Prediction (CASP) experiment (Monastyrskyy *et al.*, 2014). An additional facet of applying distinct predictors is their applicability in the in-depth analysis of a single, or a very small number of, proteins, in which the maximum accuracy with a resolution down to single residues is demanded, or the high-throughput analysis of disorder in entire genomes for comparative and evolutionary studies (Pancsa and Tompa, 2012; Schlessinger *et al.*, 2011). With a significant shift in our knowledgebase of structural disorder in DisProt (Piovesan *et al.*, 2017) that underlies predictor development, these and other features of their performance should be re-assessed. To this end, we have carried out a comprehensive comparative analysis of novel DisProt data and the performance of disorder predictors trained on prior data.

We have previously reported a large-scale analysis of ID regions in X-ray PDB structures based on over 27 000 different proteins extracted from the MobiDB database (Walsh *et al.*, 2015). In that paper, several performance measures were explored and a ranking established for a dozen fast ID predictors. Unsurprisingly, the results highlighted how methods trained on missing X-ray data generally perform better on the PDB dataset. Here, we provide a similar analysis on a dataset derived from the novel DisProt 7.0 release (Piovesan *et al.*, 2017). The analysis was carried out in the same way as before (Walsh *et al.*, 2015) and the results can be compared directly. This will help to better characterize the differences between missing X-ray residues and experimentally determined long ID regions curated from the literature.

2 Materials and methods

2.1 Datasets and classifications

The DisProt 7.0 (Piovesan *et al.*, 2017) sequences were downloaded and compared to the previous 6.02 release (Sickmeier *et al.*, 2007), providing the following seven different subsets (see Table 1). As version 7.0 is a complete re-annotation of DisProt, a ‘core’ of 488 proteins is also present in the previous release and these may have been used to train some of the predictors. It should be noted that the

Table 1. Dataset composition

DisProt	Proteins	Residues		ID regions		Fully ID
		Disorder	Ordered	Short	Long	
v 6.02	667	90 495	221 724	759	747	131
v 7.0	756	87 494	305 020	594	1408	102
Core	488	57 874	219 560	470	979	70
Complement	268	29 620	85 460	124	429	32
v 7.0 virus	70	6631	41 195	49	202	9
v 7.0 primary	581	48 996	348 518	539	637	39
v 7.0 secondary	341	59 477	333 037	55	771	84

Note: The different DisProt subsets are listed with the number of proteins, residues (disorder, order), ID regions and fully ID proteins. Short ID regions have at least five and long ID regions at least 20 consecutive residues. The DisProt v 7.0 dataset can be separated into proteins already present in DisProt v 6.02 and re-annotated (core) and new entries (complement). The last three subsets are only viral proteins (virus), proteins annotated from X-ray and NMR (primary) and indirect biochemical experiments (secondary) methods.

disorder annotation has also changed for some of these entries. The DisProt 7.0 ‘complement’ is composed of proteins not annotated in the previous release and therefore represents, in the strictest definition, data ‘unseen’ for predictors. While DisProt 7.0 always maps to a single UniProt (The UniProt Consortium, 2012) sequence, this was not necessarily the case for release 6.02, reducing the number of sequences from 694 to 667. DisProt 7.0 annotations can have a different level of confidence, ‘confident’ and ‘ambiguous’, describing confident and problematic cases respectively (Piovesan et al., 2017). In order to be conservative, ID residues are taken directly from the DisProt ‘confident’ annotations. All residues not annotated as disordered are considered ordered to limit overprediction and focus the assessment on biologically meaningful ID regions (Habchi et al., 2014). An alternative definition excluding undefined residues not annotated in DisProt and not present in the PDB is also used (see Supplementary Fig. S1 and Table S1). Multiple annotations for the same residue are consolidated into a single state (order or ID). The rationale for this conservative setup is to concentrate the prediction on bona fide ID residues in order to limit overprediction, concentrating on biologically meaningful ID regions (Habchi et al., 2014).

2.2 Predictors

Predictors were initially selected to include those of the previous assessment on the entire PDB (Walsh et al., 2015). These are (disorder definition used in parenthesis): DisEMBL (hot loops and remark 465) (Linding et al., 2003b), ESpritz (X-ray, NMR and DisProt) (Walsh et al., 2012), GlobPlot (globularity) (Linding et al., 2003a), IUPred (short and long) (Dosztányi et al., 2005), RONN (X-ray) (Yang et al., 2005) and VSL2b (combination of X-ray and Disprot) (Peng et al., 2006). This resulted in a total of ten fast predictors with different disorder flavors. Given the relatively smaller dataset size for DisProt, several recent slower predictors requiring multiple-sequence alignments were also included. These are: AUCpred (Wang et al., 2016), Disopred3 (Jones and Cozzetto, 2015), ESpritz ‘slow’ (X-ray, NMR and DisProt) (Walsh et al., 2012), Spine-D (Zhang et al., 2017), S2D (Sormanni et al., 2015) MFDp (Mizianty et al., 2010), MFDp2 (Mizianty et al., 2013) and MetaDisorder (Kozłowski and Bujnicki, 2012) in all of its flavors. Finally, MobiDB-lite (Necci et al., 2017) is included to benchmark the effects of using a consensus approach of several fast predictors.

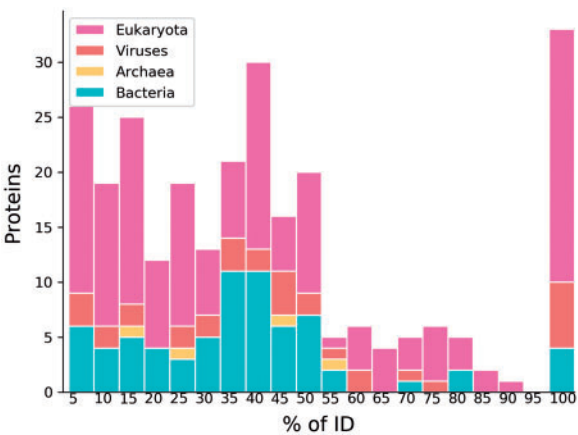


Fig. 1. Protein ID percentage distribution of the 284 new DisProt entries. The x-axis labels represent the rightmost boundaries of the bins

2.3 Performance assessment

The standard binary classification measures accuracy, sensitivity and specificity were calculated both *per residue* and as average on a *per protein* basis. The Matthews Correlation Coefficient (MCC) and AUC are used in addition for a *per residue* assessment. For the *per protein* evaluation, two disorder content measures are included, Root Mean Square Error (RMSE) and Pearson Correlation Coefficient (PCC), with predicted and observed disorder content normalized by the number of annotated residues. All performance measures are calculated as detailed in (Walsh et al., 2015). Finally, all measures are combined into a single overall ranking on which statistical significance is measured with the Welch *t*-test to determine the best methods.

3 Results

3.1 DisProt disorder is different from the PDB

Partially due to the relatively limited number of entries in previous DisProt releases, ID predictors have been usually assessed on missing X-ray residues from the PDB (Monastyrskyy et al., 2014; Walsh et al., 2015). Here, we present the first full assessment of DisProt data thanks to the newly released version 7.0 (Piovesan et al., 2017). Before starting to look at predictor performance, it is interesting to see how DisProt differs from PDB missing X-ray data. Figure 1 shows the distribution of ID in the DisProt complement divided by taxonomic kingdom. Unsurprisingly, Eukaryotic sequences are most abundant, with viruses providing an additional source of ID.

The actual ID length distribution is very different from missing X-ray coordinates in the PDB. Where PDB missing X-ray data is strongly dominated by ID regions of less than 20 residues (Walsh et al., 2015), DisProt has many proteins with a large ID fraction (Piovesan et al., 2017). In DisProt, 33 out of 284 sequences are fully disordered, which is obviously not possible in the PDB. The average ID fraction per protein in the PDB is 5.2% compared to 22.7% in DisProt and the fraction of long ID regions is 13.8% in PDB and 71.8% in DisProt. Overall, the DisProt dataset appears more representative of the natural disorder distribution in proteins. Figure 2 shows the pairwise distribution of sequence identity between DisProt sequences, peaking at ca. 10% with an average of 21%, which demonstrates the highly non-redundant nature of data in DisProt. Using a 90% cutoff, the number of DisProt 7.0 entries is just slightly reduced from 803 to 752. For comparison, the reduction in PDB entries was fourfold, from 101 338 to 24 669 (Walsh et al.,

2015). In other words, the DisProt dataset is much more diverse than PDB and sufficient to ensure an unbiased evaluation of the predictors.

3.2 Predictor performance

A large number of different ID predictors, both very fast and slower ones requiring a multiple-sequence alignment, have been benchmarked against the DisProt dataset. Results are shown (see Table 2) per protein and per residue for the complement dataset, i.e. entries

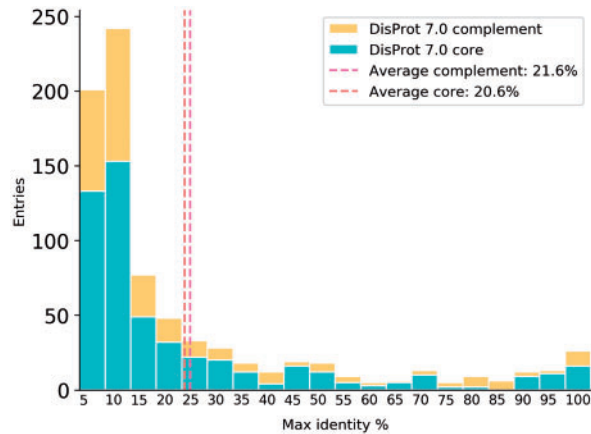


Fig. 2. DisProt pairwise identity distribution. Pairwise identity distribution for the core and complement datasets of Disprot 7.0. Identity percentage is the maximum symmetrical identity of each entry Blast results against Disprot 7.0 (see Materials and methods). The x-axis labels represent the rightmost boundary of each bin

that are not present in DisProt 6.02. This is the fairest possible benchmark, as no method was trained on the more recent DisProt entries. Results for the other three DisProt sets are similar, and not shown.

The results are coherent with the dataset differences highlighted before, i.e. long ID predictors are better on the DisProt dataset compared to the PDB. For example IUPred long is better than IUPred short and ESpritz-DisProt is better than the other ESpritz versions, in the PDB dataset the ranking is the opposite (Walsh et al., 2015). Notably, while the accuracy is somehow comparable with the PDB assessment, there is a significant change in the sensitivity and specificity. In general, for DisProt specificity decreases and sensitivity increases compared to the PDB. The AUC decrease from the PDB to DisProt is generally 5-10% (compare Table 2 with Walsh et al., 2015). This could be explained by the fact that the DisProt dataset is more balanced than PDB. It may fit better the predictor training features, with some exceptions such as methods trained on X-ray data like ESpritz X-ray. For the same reasons the PCC has improved.

In order to establish an overall ranking, the ranking for each measure has been combined. Figure 3 shows a statistical performance of the top 12 ranking representing the average of the 10 different distributions calculated on the complement dataset (see also Supplementary Fig. S2). The row methods have a worse ranking than column methods when the cell is red and *vice versa* when green. Darker colors correspond to a lower *P*-value (the number in the cells) and indicate a significant ranking difference. Interestingly, predictors using multiple sequence alignments are not significantly better than fast methods (with the exception of ESpritz-X-ray). An even stronger difference can be seen for DisEMBL 465, which was ranked first for PDB and is in the lowest quarter for DisProt.

Table 2. DisProt complement performance sorted by descending MCC

Method	Per-residue					Per-protein				
	Accuracy	Sensitivity	Specificity	AUC	MCC	Accuracy	Sensitivity	Specificity	RMSE	PCC
*ESpritz X-ray	75.10	74.41	75.79	<u>80.43</u>	45.42	65.01	64.29	65.74	07.25	<u>59.07</u>
*ESpritz DisProt	68.83	47.41	90.26	81.50	<u>41.62</u>	54.17	49.25	59.09	14.18	52.10
ESpritz DisProt	70.03	53.87	86.20	80.02	40.95	54.38	49.20	59.57	13.40	53.86
*AUCpred	70.39	57.66	83.11	72.77	39.98	62.21	60.31	64.11	08.33	53.06
*MetaDisorder	<u>72.01</u>	75.94	68.08	57.01	38.84	64.31	65.31	63.30	08.98	49.19
*MetadisorderMD	71.56	73.78	69.34	59.52	38.22	64.04	60.67	67.41	08.75	47.24
MobiDB-lite	68.31	49.98	<u>86.63</u>	76.74	38.16	56.77	33.50	80.04	09.78	57.73
IUpred long	70.73	66.83	<u>74.62</u>	75.69	37.74	60.93	50.96	70.90	08.70	53.13
*ESpritz NMR	71.37	75.18	67.56	76.7	37.69	64.81	64.72	64.90	07.51	52.37
*SPINE-D	71.43	81.89	60.97	78.64	37.47	64.20	74.70	53.70	09.71	51.22
*DISOPRED3	70.27	66.34	74.19	76.56	36.87	60.34	48.77	71.91	<u>09.46</u>	45.03
IUpred short	68.71	57.03	80.40	75.48	35.97	60.95	49.24	72.66	<u>06.96</u>	57.17
*MetadisorderMD2	70.46	77.36	63.57	69.26	35.85	64.70	65.36	64.04	09.27	45.18
ESpritz NMR	69.71	70.29	69.13	73.73	35.04	<u>62.50</u>	59.02	65.99	07.83	49.34
*MFDp2	68.08	57.32	78.84	67.73	34.34	61.58	63.11	60.05	13.28	44.33
ESpritz X-ray	67.73	55.60	79.86	75.85	34.08	60.73	51.80	69.65	06.75	59.64
VSL2b	69.35	<u>81.42</u>	57.28	76.65	33.89	62.91	<u>74.08</u>	51.74	10.42	50.08
JRONN	68.33	74.11	62.56	73.20	32.12	62.03	63.97	60.09	08.19	50.06
*MFDp	67.18	60.50	73.86	67.40	31.50	62.52	67.87	57.17	13.27	42.18
DisEMBL 465	62.88	42.12	83.64	70.39	26.77	56.74	39.55	<u>73.93</u>	07.66	58.06
*S2D	64.15	74.05	54.25	72.11	24.79	58.11	68.49	47.72	13.56	33.00
DisEMBL hot loops	61.08	58.41	63.74	65.90	19.63	56.35	58.24	54.47	08.34	41.69
GlobPlot	58.49	35.15	81.82	61.46	17.76	52.89	32.10	73.67	10.87	32.41
*Metadisorder3D	51.78	43.27	60.28	61.07	03.17	52.61	32.35	72.87	19.08	-18.65

Note: All values are shown as percentages. The top performing method in each category is shown in bold and the second best underlined. Methods marked ‘*’, rely on multiple sequence alignments. Accuracy, sensitivity and specificity are calculated per residue (left) and per protein (right). AUC and MCC are per residue. RMSE and PCC are calculated per protein and based on disorder content.

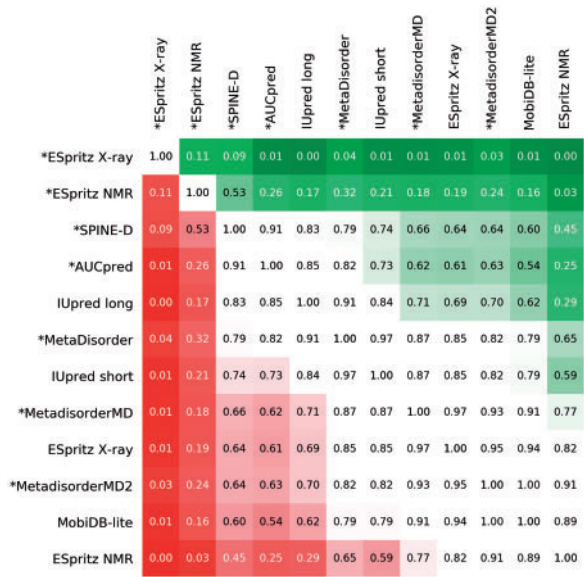


Fig. 3. Top 12 average ranking of prediction methods on the complement dataset. Methods marked ‘*’ rely on multiple sequence alignments. Methods are ranked on the basis of scores in Table 2, resulting in 10 rankings per method (ranking distribution). The Welch *t*-test *P*-value is shown inside each box as computed over all ranking distributions. Dark green background color is used if the method on the x-axis is significantly better than the one on the y-axis. Red background color is the opposite, i.e. x-axis method is significantly worse. Due to space constraints, only the top 12 methods are shown. The full figure is shown as Supplementary Figure S2 (Color version of this figure is available at Bioinformatics online.)

3.3 Performance on different subsets

One of the most interesting features of the DisProt dataset is the availability of different annotations beyond the well-known missing X-ray data from the PDB. These include NMR and especially indirect biochemical methods (termed ‘secondary’ in DisProt). Especially the longer ID regions in DisProt are dominated by secondary methods, which include a wide array of biochemical techniques providing indirect evidence for ID (Piovesan *et al.*, 2017). Albeit susceptible to some experimental errors, these provide a complementary view of ID where structural methods fail due to the intrinsic difficulty in determining ID regions. It is therefore interesting to see how the different predictors fare on these peculiar subsequences with a set of predominantly long ID regions. Figure 4 shows the performance difference between primary and secondary methods on the full DisProt 7.0 dataset sorted by decreasing MCC. Almost all predictors improve considerably, in particular those detecting long regions such as IUpred long, ESpritz-DisProt and MobiDB-lite. The ranking is also changed to the benefit of faster methods (see Fig. 4). In this case, the overall improvement can not be explained by a better balancing between positive and negative examples (as for PDB), since disorder content for secondary methods is 15.2% compared to 22.3% of the full DisProt. Conversely, the number of long regions increases from 71.8 to 94.0%. Short regions are more difficult to predict and a higher number of regions increase the probability of making errors.

Figure 5 shows the same analysis performed on the subset of viral proteins. Viral proteins are known to have extensive disorder, due to the evolutionary pressure on having a compact genome with high functional density, combined with an ability to evade the immune system (Davey *et al.*, 2011). Similarly to secondary methods this dataset is enriched in long regions (81.2%). In this case the

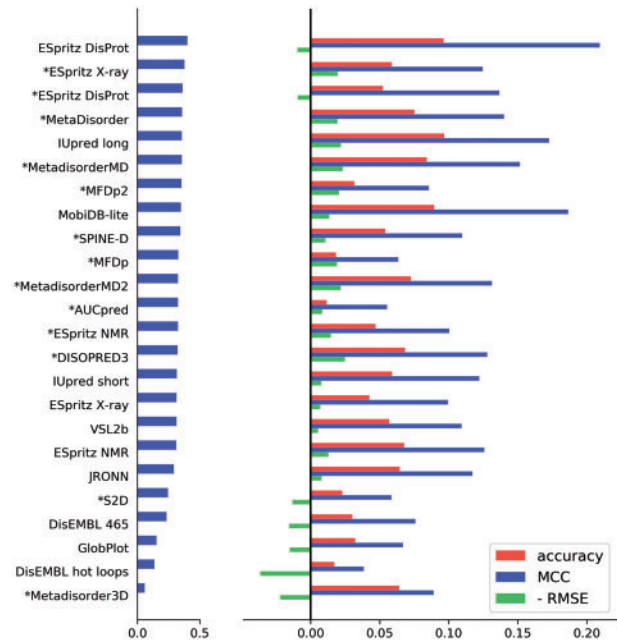


Fig. 4. Difference in performance between secondary and primary methods on the full DisProt 7.0. Methods are ordered by decreasing MCC on the DisProt 7.0 secondary dataset, shown left. On the right panel, the x-axis represents the improvement of secondary over primary methods. Accuracy is scaled in the [0–1] range. The delta RMSE is negative to follow the x-axis direction. Methods marked ‘*’ rely on multiple sequence alignments

improvement is less relevant and there is not a clear distinction between long and short predictors. Instead, a contribution to the improvement, even if weak, can be related to evolutionary information since all the three different ESpritz flavors improve when exploiting conservation. These observations probably relate to the higher rate of evolutionary variation of viral proteins, which attests to how structural disorder can combine functionality with relaxed evolutionary selection pressure (Xue *et al.*, 2014).

3.4 Consensus of disorder predictions

Given the similar performance of several ID predictors, it is worth investigating how much these agree on the actual regions of disorder. To this end, we evaluated the consensus among ten fast ID predictors (three ESpritz, two DisEMBL and two IUpred flavors, plus GlobPlot, VSL2b and RONN) in terms of their agreement on defining ID regions. To be more statistically significant, the evaluation was carried out on the entire DisProt 7.0 dataset. Figure 6 shows how only a strong majority of at least 8 out of 10 methods labeling a region ID has a probability of over 50% of being correct. Perhaps more troubling, only about a third of the total ID residues are covered by this consensus approach. A similar proportion of ID residues has an intermediate number (i.e. 4–7) of predictors agreeing and the rest goes virtually undetected. In other words, while the predictors have similar overall performances, the actual ID residues being predicted are quite divergent and a large fraction of ID remains undetected. These results are still encouraging, as more ID was left undetected in the PDB (Walsh *et al.*, 2015). It would appear that the predictors have gathered a basic understanding of the sequence signal for ID, but are rather fuzzy on cases closer to the classification boundary. This is probably due to the lack of good training data which will improve as more high-quality ID annotation becomes available. Overall, this situation suggests that

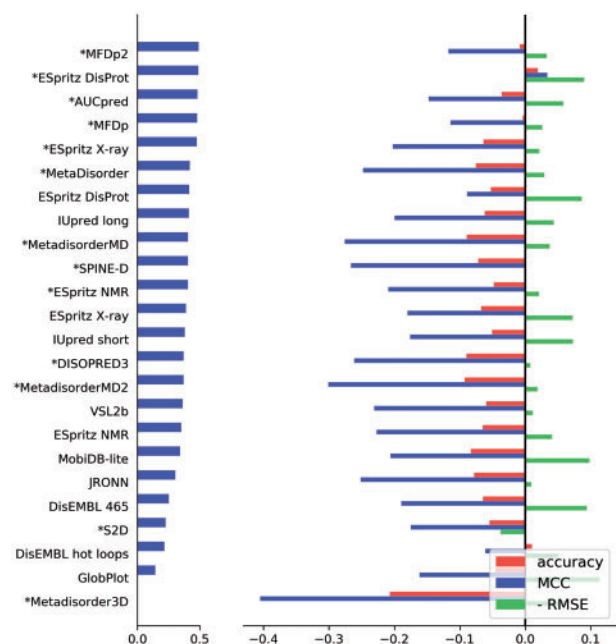


Fig. 5. Difference in performance between viral and non-viral proteins on the full DisProt 7.0 dataset. Methods are ordered by decreasing MCC on the viral DisProt 7.0 dataset, shown left. On the right panel, the x-axis represents the improvement on viral over non-viral proteins. Accuracy is scaled in the [0–1] range. The delta RMSE is negative to follow x-axis direction. Methods marked '*' rely on multiple sequence alignments

combining several fast ID predictors using a stronger majority threshold can provide good results and explains the performance of MobiDB-lite (Necci et al., 2017).

3.5 ID versus non-structure prediction

The ID definition used in DisProt prediction focuses on regions where disorder is thought to be functionally relevant (Piovesan et al., 2017). Many disorder predictors instead are trained to recognize missing residues in X-ray PDB structures as a proxy for ID. In-between may exist undefined residues, which are neither bona fide ID (in DisProt) nor structured (in the PDB; see Supplementary Fig. S1). Indeed, 53.2% of residues in the DisProt 7.0 dataset fall in the undefined category (see Supplementary Fig. S3). Repeating the assessment excluding undefined residues yields overall consistent results, with two points standing out. The specificity of several predictors trained on X-ray data and using multiple sequence alignments is increased by up to 20% with consequent increases in AUC and MCC (see Supplementary Table S2). As the specificity increase is uneven between predictors, the ranking also fluctuates (see Supplementary Figs S4–S6).

This may suggest either that the assessment is biased or that the predictors are not specifically trained to recognize ID. To help elucidate the difference, we plot the amino acid composition of the different residue types in Figure 7. The composition for disorder and structure follow well-established opposite trends, with lack of hydrophobic and increase in charged residues denoting ID. Undefined residues however are generally close to the dataset average and resemble structure more than ID. This suggests that functional ID regions are a separate phenomenon, which stand out with a different amino acid composition as opposed to being just the contrary of structure. This may also help explain differences in ranking between the assessment with or without undefined residues. The

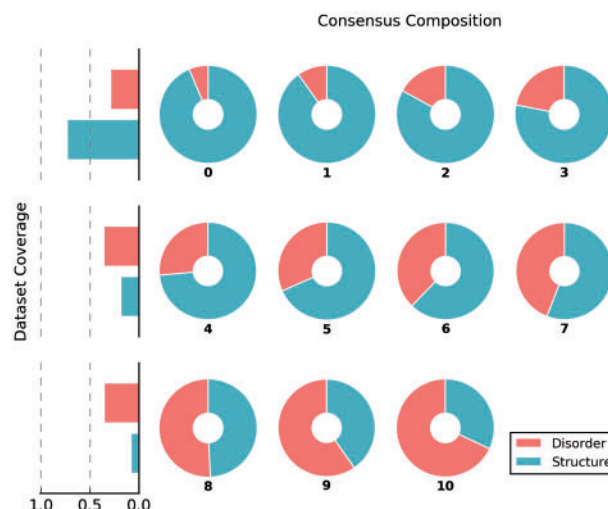


Fig. 6. Proportion of disordered and structured residues in DisProt 7.0 annotation as a function of ten methods predicting disorder. Each pie chart shows the fraction of disorder and structure at a given number of methods predicting a certain residue as disordered, ranging from 0 (i.e. none) to 10. The bar plots on the left aggregate data for each row showing the dataset coverage. This is the sum of structured and disordered residues of the row divided by the total number of structured or disordered residues in the dataset

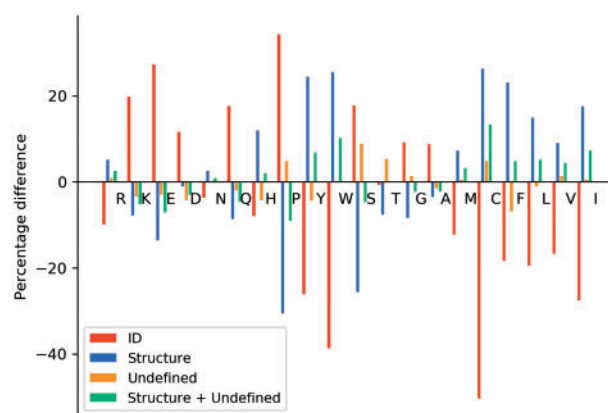


Fig. 7. Distribution of the twenty amino acids in different fractions of the DisProt complement dataset. Amino acids are shown in increasing Kyte-Doolittle hydrophobicity from left to right. The percentage of enrichment is calculated using the entire dataset as reference. Notice how disorder and structure are complementary. Undefined residues are broadly comparable to structure but generally closer to average, with the exceptions of serine and threonine

upshot from this subtle difference is that many ID predictors, trained on X-ray structure data with limited ID, are likely predicting the absence of structure instead. This is understandable given the previous lack of bona fide ID regions in large enough numbers but highlights an opportunity for future improvement.

4 Discussion

We have presented the first evaluation of a large number of ID predictors on a large curated set of proteins experimentally determined to be intrinsically disordered. This was possible due to the recent upgrade of the DisProt database (Piovesan et al., 2017). Previous critical assessments for ID prediction were based on missing X-ray data

from PDB structures (Monastyrskyy *et al.*, 2014; Walsh *et al.*, 2015). In CASP, this situation has been acknowledged as being not optimal (Monastyrskyy *et al.*, 2014) and ultimately led to the discontinuing of the disorder prediction category. In contrast, the DisProt 7.0 dataset provides just the type of long disorder important for protein function. This difference is exemplified by the significantly higher fraction of long ID regions in DisProt (71.8%) compared to the PDB (13.8%). Hence, the benchmarking results we obtained were far from obvious.

In order to allow a fair comparison to previous results based on the PDB, the analysis and performance measures were chosen to be identical to our previous work (Walsh *et al.*, 2015). The results have been overall consistent, as ID predictors are clearly able to recognize the longer disordered regions from the DisProt dataset. In terms of several performance measures, results are comparable to those obtained in the PDB. However, a few trends emerge.

First of all, the actual ranking is different depending on whether predictors are benchmarked on DisProt or PDB data. E.g. DisEMBL 465 was performing well on PDB data (Walsh *et al.*, 2015), but is now in the lowest quarter of the ranking. Other methods trained on longer ID regions (e.g. IUPred-long) perform better than on the PDB. This is compounded when looking at specific subsets of the DisProt 7.0 data, such as secondary methods or viral proteins. Here, the ranking is further changed compared to the PDB dataset. It appears that the ID predictors are able to capture a strong signal for disorder in the sequence, but are not well trained on subtler cases such as non-ID residues outside X-ray structures. In fact, a lot of ID in the dataset still goes undetected (see Fig. 6). This may also help explain the previously noted decrease in ID predictor performance when predicting entire UniProt sequences (Walsh *et al.*, 2015).

As second interesting observation is the difference between ‘fast’ (i.e. single-sequence) methods able to predict ID for a typical protein sequence in less than a second compared to those requiring multiple sequence alignments (typically from Blast) as input. The latter have proven quite popular in the literature, e.g. Jones and Cozzetto (2015), Sormanni *et al.* (2015), Wang *et al.* (2016) and Zhang *et al.* (2017), but are generally three orders of magnitude slower than ‘fast’ methods (Walsh *et al.*, 2012). Our benchmarking on DisProt shows that the difference in performance is probably not sufficient to justify the severe reduction in speed for most applications. Indeed, training on more high quality data is likely to provide a larger performance gain.

In conclusion, the benchmarking of ID predictors on DisProt 7.0 has provided interesting results which we anticipate will give food for thought to methods developers. Acknowledging the subtle difference between ID and other regions outside X-ray structures is a first step. The observed significant differences in changes of predictor performance upon updating DisProt data warrants that structural disorder does come in different flavors, and a continuous improvement of both data quality/consistency, and disorder predictors is necessary for improving consistency of our concepts of structural disorder. To assist in these efforts, as the analysis pipeline is straightforward to execute on future DisProt updates, we plan to run similar assessments periodically to help the user community understand the strengths and limits of predictors for intrinsic disorder. We encourage interested developers to contact us if they would like their method to be included in the future.

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