

Methodology article

Open Access

Application of amino acid occurrence for discriminating different folding types of globular proteins

Y-h Taguchi*^{1,2} and M Michael Gromiha*³

Address: ¹Department of Physics, Faculty of Science and Technology, Chuo University, 1-13-27 Kasuga, Bunkyo-ku, Tokyo 112-8551, Japan, ²Institute for Science and Technology, Chuo University, 1-13-27 Kasuga, Bunkyo-ku, Tokyo 112-8551, Japan and ³Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST), AIST Tokyo Waterfront Bio-IT Research Building, 2-42 Aomi, Koto-ku, Tokyo 135-0064, Japan

Email: Y-h Taguchi* - tag@granular.com; M Michael Gromiha* - michael-gromiha@aist.go.jp

* Corresponding authors

Published: 22 October 2007

Received: 1 June 2007

BMC Bioinformatics 2007, 8:404 doi:10.1186/1471-2105-8-404

Accepted: 22 October 2007

This article is available from: <http://www.biomedcentral.com/1471-2105/8/404>

© 2007 Taguchi and Gromiha; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract

Background: Predicting the three-dimensional structure of a protein from its amino acid sequence is a long-standing goal in computational/molecular biology. The discrimination of different structural classes and folding types are intermediate steps in protein structure prediction.

Results: In this work, we have proposed a method based on linear discriminant analysis (LDA) for discriminating 30 different folding types of globular proteins using amino acid occurrence. Our method was tested with a non-redundant set of 1612 proteins and it discriminated them with the accuracy of 38%, which is comparable to or better than other methods in the literature. A web server has been developed for discriminating the folding type of a query protein from its amino acid sequence and it is available at <http://granular.com/PROLDA/>.

Conclusion: Amino acid occurrence has been successfully used to discriminate different folding types of globular proteins. The discrimination accuracy obtained with amino acid occurrence is better than that obtained with amino acid composition and/or amino acid properties. In addition, the method is very fast to obtain the results.

Background

Deciphering the native conformation of a protein from its amino acid sequence, known as, protein folding problem is a challenging task. The recognition of proteins belonging to same fold/structural class is an intermediate step to protein structure prediction. For the past few decades, several methods have been proposed for predicting protein structural classes. These methods include discriminant analysis [1], correlation coefficient [2], hydrophobicity profiles [3], amino acid index [4], Bayes decision rule [5], amino acid distributions [6], functional domain occurrences [7], supervised fuzzy clustering approach [8] and

amino acid principal component analysis [9]. These methods discriminated protein structural classes with the sensitivity of 70–100% and it mainly depends on the data set. Wang and Yuan [5] developed a data set of 674 globular protein domains belonging to four different structural classes and reported that methods claiming 100% sensitivity for structural class prediction could predict only with the sensitivity of 60% with this data set.

On the other hand, alignment profiles have been widely used for recognizing protein folds [10,11]. Recently, Cheng and Baldi [12] proposed a machine learning algo-

rithm for fold recognition using secondary structure, solvent accessibility, contact map and β -strand pairing, which showed a pair wise sensitivity of 27%. On the other hand, amino acid properties have been used for discriminating membrane proteins [13], identification of membrane spanning regions [14], prediction of protein structural classes [15], protein folding rates [16], protein stability [17] etc. Towards this direction, Ding and Dubchak [18] proposed a method based on neural networks and support vector machines for fold recognition using amino acid composition and five other properties, and reported a cross-validated sensitivity of 45%. Further, Ofra and Margalit [19] showed the existence of significant similarity in amino acid composition between proteins of the same fold. In this work, we have used amino acid occurrence (not composition) for discriminating 30 different folding types of globular proteins. We have developed a method based on linear discriminant analysis (LDA), which discriminated a set of 1612 proteins with an accuracy of 38%, which is comparable to other methods in the literature, in spite of the simplicity of the method and large dataset.

Results and discussion

Role of re-weighting for fold discrimination

We have computed the occurrence of all the 20 amino acid residues in each protein, which represents the elements of 20 dimensional vectors in each protein. We have applied LDA to these vectors for discrimination. We have employed two kinds of LDA, i.e., with and without re-weighting. In LDA with re-weighting, i.e. $W_k = 1$ in eq. (1), all folds equally contribute to maximize the performance of discrimination irrespective of the number of proteins in each fold; i.e., if one fold has hundreds of proteins and another has only few proteins, LDA is optimized to achieve the highest performance equally in all folds. This re-weighting is important especially when the number of proteins included in each fold has large variations. On the other hand, LDA without re-weighting, i.e. $W_k = N_k$ in eq. (1), tends to achieve the maximum performance for the whole dataset.

We have used the measures, accuracy, sensitivity, precision and F1 for examining the performance of the method. In general, accuracy has the tendency to show high values without re-weighting since it is computed

with all data. Sensitivity tends to increase by re-weighting, giving equal weight to each fold. In contrast, precision has the tendency to decrease by re-weighting, since re-weighting increase FP for folds with less number of proteins. On the other hand, F1 is independent of re-weighting as it is harmonic mean of sensitivity and precision.

In Table 1, we presented the discrimination results obtained with different measures and two kinds of LDA (with and without re-weighting). As expected, re-weighting significantly changed all the performances other than F1. Re-weighting increased the sensitivity whereas an opposite trend was observed for precision and accuracy. This is due to the divergence in the number of proteins in each fold (min. 25, max. 173, mean 54, see Table 2). F1 does not change significantly by re-weighting.

Remarkably, we achieved the accuracy of 38% (without re-weighting), which is the best performance to our knowledge, for large number of folds (30) and proteins (1612). Further, the method is extremely simple, which indicates that the amino acid occurrence of proteins carry sufficient information to discriminate protein folds.

Discrimination of proteins belonging to different folding types

We have examined the ability of the present method for predicting proteins belonging to 30 major folds. In Table 2, we have shown the performances of discriminating 30 different folds. We observed that the folds with less number of proteins have the sensitivity of less than 10% without re-weighting. For example, SAM domain like fold has the sensitivity of 8%, which has only 26 proteins. Similar tendency is also observed for the folds b.2, b.34, c.3, c.47, c.55, d.15 and d.17. The sensitivity of these folds increased significantly with re-weighting. On the other hand, many folds with less than 30 proteins have the sensitivity of more than 20% without re-weighting (e.g., a.3, a.24, a.39 etc.). As there are 30 folds, the expected sensitivity is only 3.3% if classification is supposed to be random. In Table 2, we have also shown the ratio between the number of proteins in each fold and the total number of proteins, which ranges from 2 to 11%. Hence the sensitivity of 20% obtained for several folds is significantly higher than that of random for fold discrimination. Interestingly, most of the folds that were discriminated with more than

Table 1: Role of re-weighting. Leave-one-out cross validation results [%] obtained with different measures and two types of LDA

	with re-weighting				without re-weighting			
	sensitivity	precision	F1	accuracy	sensitivity	precision	F1	accuracy
Occurrence	33	29.	29	33	28	35	30	38
Composition	27	23	23	26	24	27	27	33

Table 2: Performances of fold recognition. Leave-one-out cross validation performances [%] in each fold. wo: without re-weighting, w: with re-weighting

ID	Fold	Fold Description	Number	Ratio	Sensitivity		Precision		F1	
					wo	w	wo	w	wo	w
all- α										
1	a.3	Cytochrome C	25	2	24	48	50	27	32	35
2	a.4	DNA/RNA binding 3-helical bundle	103	6	73	49	43	51	54	50
3	a.24	Four helical up and down bundle	26	2	23	38	35	20	28	26
4	a.39	EF hand-like fold	25	2	40	44	45	26	43	33
5	a.60	SAMdomain-like	26	2	8	27	29	12	12	16
6	a.118	α - α superhelix	47	3	47	45	50	50	48	47
all- β										
7	b.1	Immunoglobulin-like β -sandwich	173	11	76	38	41	69	54	49
8	b.2	Common fold of diphtheria toxin/transcription factors/ cytochrome f	28	2	4	29	11	21	5	24
9	b.6	Cupredoxin-like	30	2	27	37	42	22	33	27
10	b.18	Galactose-binding domain-like	25	2	20	36	50	26	29	30
11	b.29	Concanavalin A-like lectins/glucanases	26	2	23	27	24	18	24	22
12	b.34	SH3-like barrel	42	3	0	29	0	20	-	24
13	b.40	OB-fold	78	5	22	24	24	24	23	24
14	b.82	Double-stranded α -helix	34	2	12	18	19	17	15	17
15	b.121	Nucleoplasmin-like	42	3	52	52	51	47	52	49
$\alpha\beta$										
16	c.1	TIM barrel	145	9	44	27	57	65	50	38
17	c.2	NAD(P)-binding Rossmann-fold domains	77	5	34	31	30	32	32	32
18	c.3	FAD/NAD(P)-binding domain	31	2	10	16	13	11	11	13
19	c.23	Flavodoxin-like	55	3	11	5	17	8	13	7
20	c.26	Adenine nucleotide a hydrolase-like	34	2	12	29	14	22	13	25
21	c.37	P-loop containing nucleoside triphosphate hydrolases	95	6	43	34	42	53	43	41
22	c.47	Thioredoxin fold	32	2	9	19	38	10	15	13
23	c.55	Ribonuclease H-like motif	49	3	4	6	11	8	6	7
24	c.66	S-adenosyl-L-methionine-dependent methyltransferases	34	2	29	29	31	21	30	24
25	c.69	$\alpha\beta$ -Hydrolases	37	2	35	41	39	34	37	37
$\alpha + \beta$										
26	d.15	β -Grasp, ubiquitin-like	42	3	5	21	40	18	9	19
27	d.17	Cystatin-like	25	2	0	8	-	4	-	5
28	d.58	Ferredoxin-like small	118	7	32	7	17	25	22	11
small										
29	g.3	Knottins	80	5	98	89	72	82	83	85
30	g.41	Rubredoxin-like	28	2	11	71	75	32	19	44

20% sensitivity belong to either all- α or all- β class. This might be due to the fact that these proteins have different secondary structural patterns and hence they are easy to discriminate them. In addition, folds in each of these classes are near-by each other in amino acid occurrence vector space, which caused high sensitivity. On the other hand, an opposite tendency was observed for precision. Re-weighting decreased the precision for several folds including a.3, a.24, a.29, a.60, b.6, b.18, b.29, c.23, c.47, d.15, and g.41. Most of these folds have less number of proteins.

The re-weighting procedure causes two opposite effects: increased the sensitivity and decreased the precision. Hence, F1 may be used to balance these effects. Only two folds, c.23 and d.58 decreased the F1 with re-weighting

and several folds significantly increased the F1 by re-weighting (e.g. b.2, b.34, c.26, d.17, and g.41).

The comparison between experimental versus predicted folds is shown in Fig. 1. In this figure, dark block indicates the presence of many proteins. The data are normalized in such a way that the total percentage of true fold is 100%. Fig. 1a showed that mainly the folds with more number of proteins are misclassified without re-weighting (e.g., a.4, b.1, c.1 and d.58). The trend has been changed after re-weighting: the misclassified proteins are observed to be within the same structural class. Especially, in $\alpha + \beta$ class, the block diagonal region is distributed almost uniformly, which is partially caused by re-weighting. Since each fold is equally weighted, $\alpha + \beta$ class is less weighted than other classes. This causes inter-class misclassification between α

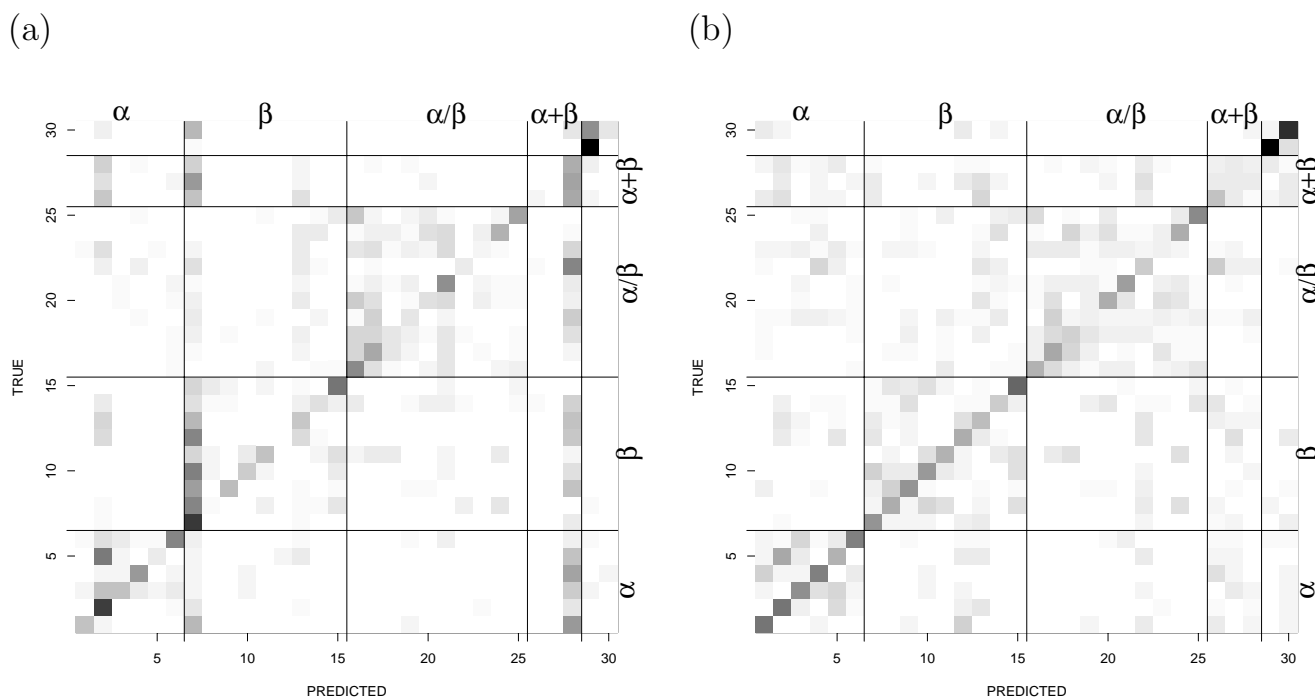


Figure 1

Prediction versus experiment. Comparison between predicted and experimental folds in 1612 proteins. The diagonal elements show the correctly predicted proteins. Dark block indicates the presence of more number of proteins and solid line indicates the boundary between five classes as shown in Table 2, i.e., all- α , all- β , α/β , and $\alpha + \beta$ and small proteins. (a) without re-weighting. (b) with re-weighting.

$+ \beta$ and other classes, because $\alpha + \beta$ class has only three folds. However, two folds in small structural class can be discriminated with high accuracy/sensitivity/precision/F1 and $\alpha + \beta$ folds are difficult to discriminate using our method.

Comparison among different re-weighting procedures

The results presented in Tables 1 and 2 showed that the sensitivity of discriminating protein folds differs significantly between different methods (with and without re-weighting). Hence, it would be difficult to choose the best method for fold recognition. However, it may be selected based on the interest of the users, whether the prediction is optimized for each fold or over all dataset.

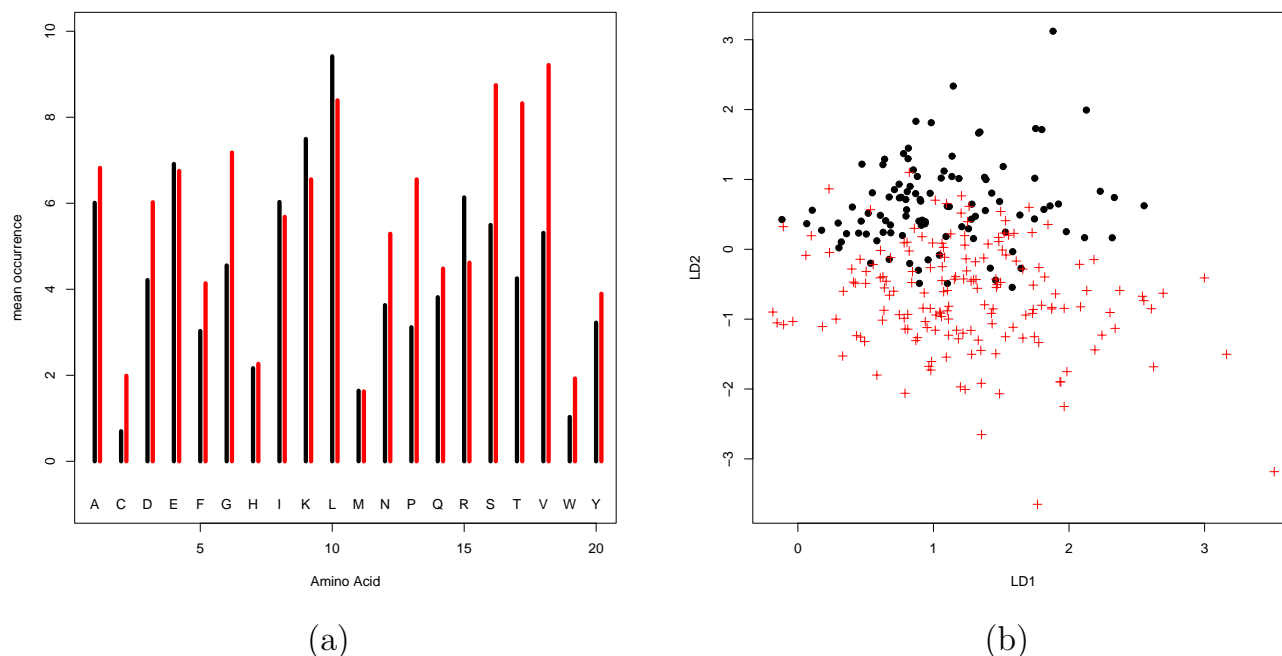
Usually, training and test sets of data are obtained from sequence and structure databases and are culled with sequence identity. However, these data sets do not always reflect proper representatives of all proteins in different folds, e.g., protein population in each fold. Further, the proteins available in databases such as, PDB are biased with the proteins that can be solved experimentally, which may be different from the proportion of real proteins. Hence, considering these aspects would help to

develop "good" methods for protein fold recognition in future.

In essence, based on the methods and data sets used in the present work, we suggest that the performance with re-weighting is better than that without re-weighting.

Influence of amino acid occurrence in recognizing protein folds

The importance of amino acid occurrence is illustrated with Figure 2(a). In this figure we show the occurrence of the 20 types of amino acid residues in DNA/RNA binding 3-helical bundle (a.4) and Immunoglobulin-like β -sandwich (b.1). The average number of amino acid residues in these folds are 88 and 110, respectively. We observed that the residues Gly, Pro, Ser, Thr and Val are dominant in the fold b.1 whereas an opposite trend was observed for Leu and Arg. In Figure 2(b), we have shown the distribution of residues in "amino acid occurrence" space. It is clearly seen that the two folds are more or less separated in this space. We observed similar results about the variation of amino acid occurrences among different folds in our data set.

**Figure 2**

Amino acid occurrence. (a) Comparison between mean amino acid occurrence of two typical folds, DNA/RNA binding α -helical bundle (a.4, black) and Immunoglobulin-like β -sandwich (b.2, red) (b) Distribution of these two folds over the first two discriminant functions with re-weighting. a.4: filled black circles, b.2: red crosses.

In addition, we have tested the performance of the method using amino acid composition (i.e., amino acid occurrence/total number of residues) in each protein. We noticed that the accuracy without re-weighting decreased to 33% indicating the importance of amino acid occurrence (un-normalized composition) in each fold (Table 1). Similar tendency is also observed for discriminating β -barrel membrane proteins [16]. Hence, we suggest that the amino acid occurrence is better than composition for discriminating protein folds. In fact, the normalization of amino acid composition produced the problem of co-linearity, i.e., diversity of vectors is not sufficient compared with the number of proteins. The reason for the dependency of F1 upon different types of LDA (with or without re-weighting) is that four folds have no positive proteins without re-weighting. On the other hand, amino acid occurrence has only two folds without any positive proteins (without re-weighting) as seen in Table 2.

Probability measure of discrimination

In order to have the feasibility of combining the results of our method with other methods we provided the probability of being a protein in a specific fold along with the predicted folding type. In Figure 3, we have shown the probability for fold a.4 (DNA/RNA binding 3-helical bun-

dle). Clearly, the fold a.4 has the highest average probability. However, some other folds, (e.g., a.60, d.15, d.17 and d.58) have relatively higher probabilities. This may result in wrong discrimination, which may be fixed by combining the results with other methods.

Comparison with other methods

We have compared the performance of our method with other related works in the literature. Ding and Dubchak [18] introduced a combined method for predicting the folding type of a protein. They have used six parameters, amino acid composition, secondary structure, hydrophobicity, van der Waals volume, polarity and polarizability as attributes, and neural networks and support vector machines for recognition. These features have been combined with the number of votes in each method. They reported the sensitivity of 56% in a test set of 384 proteins and 10-fold cross validation sensitivity of 45% in a training set of 311 proteins from 27 folding types. We have used the same dataset of 311 proteins and assessed the performance of our method. We observed that our method could predict with the leave-one-out cross validation accuracy of 42% (with LDA without re-weighting), which is close to that (45%) reported in Ding and Dubchak [18].

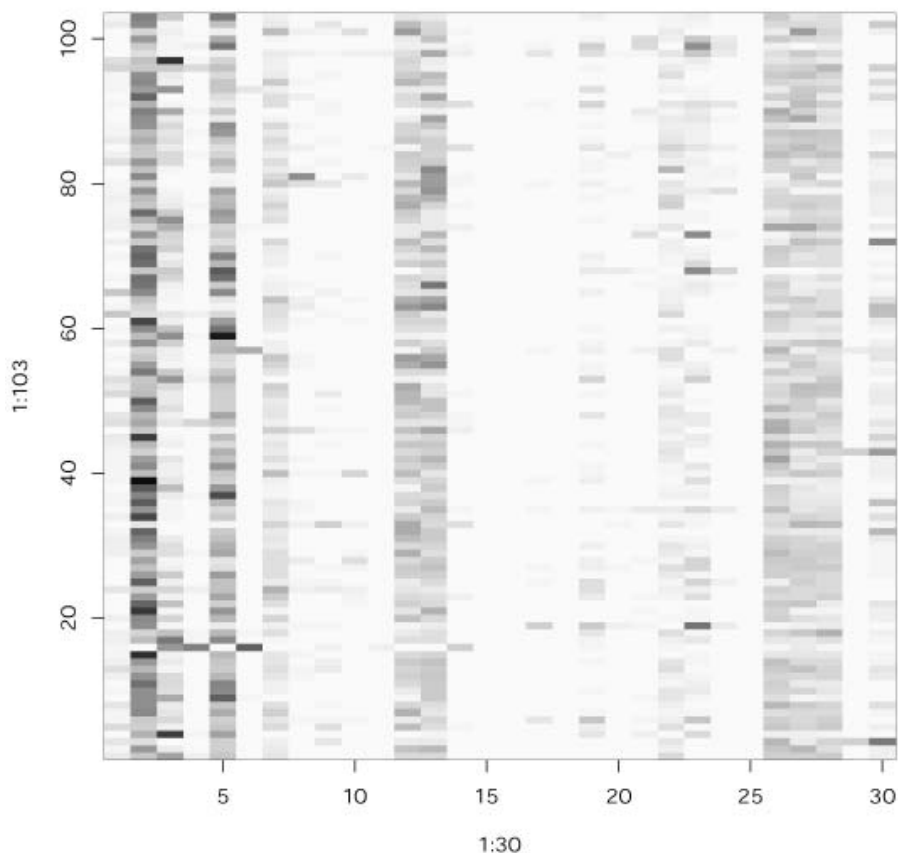


Figure 3

Probability measure of discrimination. Rows : 103 proteins in fold (a.4). Columns : 30 folds. From left to right, the order is ID in Table 2. The darkest square corresponds to probability 0.5, and the lightest is zero.

In addition, we have selected the proteins from the folds that are common in both the studies and tested the performance of our method (trained with our dataset of 1612 proteins) in predicting the folding types of the proteins used in Ding and Dubchak [18]. The results are presented in Table 3. Interestingly, our method with re-weighting could correctly identify the folding types with F1 value of more than 30% in 11 among the 19 considered folds. The performances are similar to or better than that reported with the dataset of 1612 proteins. Although our method is optimized with different datasets it has the power to predict the folding type of independent dataset of proteins with similar sensitivity.

Further, there are several advantages in our method: (i) only one feature, amino acid occurrence is sufficient for prediction rather than six features. The comparison of

results obtained with only one feature showed that the performance of our method (42%) is significantly better than that of Ding and Dubchak [18] reported with amino acid composition (20–49%), (ii) voting procedure is not necessary; our method can be directly used for multi-fold classifications, (iii) our method uses LDA, which requires significantly less computational power compared with SVM. In SVM one has to diagonalize the matrix with the size of (protein number) \times (protein number); on the other hand, LDA requires only diagonalization of 20 (the number of kinds of amino acid residues) \times 20 matrix independent of number of proteins and (iv) although they have reported the dependency of fold specific sensitivities upon number of proteins in each fold, it is difficult to compensate this effect without modifying the complicated voting systems; our method has freedom to compensate it as discussed in the previous sections.

Table 3: Performances with independent dataset Predictive ability [%] of our method to the independent dataset of proteins used in Ding and Dubchak [18]. wo: without re-weighting, w: with re-weighting

Fold Description	Number	Ratio [%]	Sensitivity		Precision		F1	
			wo	w	wo	w	wo	w
Cytochrome C	16	3	56	94	64	47	60	63
DNA/RNA binding 3-helical bundle	32	6	75	56	41	47	53	51
Four helical up and down bundle	15	3	33	33	71	42	45	37
EF hand-like fold	15	3	53	53	57	42	55	47
Immunoglobulin-like β -sandwich	74	14	66	31	44	68	53	43
Cupredoxin-like	21	4	29	38	50	33	36	36
Concanavalin A-like lectins/glucanases	13	2	38	38	42	33	40	36
SH3-like barrel	16	3	0	50	-	44	-	47
OB-fold	32	6	16	28	26	31	20	30
TIM barrel	77	14	40	25	66	70	50	37
FAD/NAD: (P)-binding domain	23	4	22	30	114	50	37	38
Flavodoxin-like	24	5	8	13	28	35	13	18
NAD: (P)-binding Rossmann-fold domains	40	8	40	35	5	8	8	13
P-loop containing nucleoside triphosphate hydrolases	22	4	23	18	38	50	29	27
Thioredoxin fold	17	3	18	35	33	25	23	29
Ribonuclease H-like motif	22	4	5	18	14	22	7	20
α/β -Hydrolases	18	3	33	39	43	41	38	40
β -Grasp, ubiquitin-like	15	3	0	33	0	20	-	25
Ferredoxin-like	40	8	23	3	11	10	15	4
Total/Mean	532		31	35	42	38	34	34
Accuracy								
without reweighting			36					
with reweighting			32					

Recently, Shen and Chou [20] reported better sensitivity for the same data set of Ding and Dubchak [18]. However, the results are biased with training set of data. We have evaluated the sensitivity of identifying proteins belonging to the folds, four helical up and down bundle (a.24) and EF hand-like (a.39) and we observed that the sensitivity is 30.5% and 24%, respectively. Our predicted sensitivities (38% and 44%, with re-weighting, see table 2) are better than that of Shen and Chou [20].

Possible reasons for obtaining good performance with amino acid occurrence

We have analyzed the possible reasons for obtaining good performance with amino acid occurrence. In Table 4, we have summarized the performance as a function of different features. When we use more than two features to discriminate folds, we simply apply LDA to merge feature vectors. This means, if there are two features vectors \vec{f}_n with n components and \vec{f}_m with m features,

$$\vec{f}_n = (f_{n1}, f_{n2}, \dots, f_{nn})$$

$$\vec{f}_m = (f_{m1}, f_{m2}, \dots, f_{mm}),$$

then we merge and apply LDA to

$$\vec{f}_{m+n} = (f_{n1}, f_{n2}, \dots, f_{nm}, f_{m1}, f_{m2}, \dots, f_{mm}).$$

The usage of five features, i.e., predicted secondary structure, hydrophobicity, normalized van der Waals volume, polarity, polarizability [18] along with amino acid composition yielded the accuracy of 45% using sophisticated and time consuming methods. On the other hand, our simple method employing amino acid occurrence and five features has also showed almost the same value (44%).

The in-depth analysis of the results presented in Table 4 revealed many interesting features. For example, amino acid composition alone showed the accuracy of 35%, which is 7% less than that obtained with occurrence (42%). On the other hand, composition and length (i.e., the first 20 components of feature vectors consist of composition and the 21th component is amino acid length) increased the accuracy from 35% to 38%. The composi-

Table 4: Performances with other features Mean performances [%] obtained with different features for the data set used in Ding and Dubchak [18]. Re-weighting scheme is employed

	Sensitivity	Precision	F1	Accuracy
Features				
secondary structure	35	32	40	36
polarity	19	18	26	21
polarizability	18	18	26	19
hydrophobicity	23	22	28	24
volume	21	20	25	22
Composition				
composition	34	33	34	35
composition + length	36	35	38	38
composition + other five features	35	39	39	39
Occurrence				
occurrence	40	40	39	42
occurrence + other five features	40	46	42	44

tion and five features showed the accuracy of 39%, which is similar (38%) to that obtained with composition and length. Hence, length of the protein has an important role as that of five features for discriminating protein folds. This analysis demonstrates the importance of amino acid length and obtaining good performance with amino acid occurrence.

As an individual feature amino acid occurrence showed the best performance among all features, including secondary structure. The combination of amino acid occurrence with other features did not increase the sensitivity and the increase of other parameters is only marginal. This result reveals that the amino acid occurrence contains most of the information that are reflected in other physical features.

Generally, any physical feature can be expressed by amino acid occurrence. Hence, linear combination of amino acid occurrence may express many of physical properties of proteins. In order to verify this concept, we have computed the correlation coefficients between 49 amino acid properties [21-23] and the first discriminate function. Each property consists of 20 dimensional vector, like

$$\tilde{p}^k = (P_1^k, P_2^k, \dots, P_i^k, \dots, P_{20}^k),$$

where P_i^k is the k th physical property of i th amino acid. Since discriminant function is also 20 dimensional vector and each component of which describes contribution

from each amino acid, one can compute correlation coefficient between them.

As can be seen in Table 5, 23 out of 49 properties have high correlation coefficients and less than 5% q -values (i.e., FDR corrected p -values). This analysis shows that linear discriminant function can express many of physical properties, at least, partly. Hence, even if we do not consider physical properties directly, the consideration of amino acid occurrence could discriminate folds well.

Fold recognition on the web

We have developed a web server for discriminating protein folds from amino acid sequence [24]. It takes the amino acid sequence as input and displays the folding type in the output along with probability. Further, the server has the feasibility of selecting the method, with and without re-weighting, and the display options to show the probability details for each fold.

Advantages and limitations of the method

The main advantage of the present method is the discrimination of 30 different folding types of globular proteins with high accuracy/sensitivity/precision/F1. Further it will provide the probability of being a protein in a specific fold. The discrimination results along with probability may be helpful to select templates to build models to new protein. Further, it can be combined with other methods for better performance. The limitation of the method is the usage of only 30 specific folds for discrimination.

Table 5: Correlation between physical properties and the first discriminant function Brief descriptions of 49 selected physico-chemical, energetic and conformational properties, their correlation coefficient with the first discriminate function, and q-value. Asterisks in the last column shows q-value is less than 5%

No.	Description	Corr. Coef.	q-value [%]	q ≤ 5%
1.	Compressibility	0.04	38.6	
2.	Thermodynamic transfer hydrophobicity	0.54	1.9	*
3.	Surrounding hydrophobicity	0.74	0.4	*
4.	Polarity	0.36	9.2	
5.	Isoelectric point	0.02	41.2	
6.	Equilibrium constant with reference to the ionization property	0.01	41.7	
7.	Molecular weight	0.06	38.4	
8.	Bulkiness	0.49	3.0	*
9.	Chromatographic index	0.51	2.7	*
10.	Refractive index	0.36	9.2	
11.	Normalized consensus hydrophobicity	0.48	3.4	*
12.	Short and medium range non-bonded energy	0.11	32.7	
13.	Long-range non-bonded energy	0.65	0.7	*
14.	Total non-bonded energy	0.57	1.5	*
15.	Alpha-helical tendency	0.29	14.1	
16.	Beta-helical tendency	0.63	0.8	*
17.	Turn tendency	0.61	0.9	*
18.	Coil tendency	0.60	1.1	*
19.	Helical contact area	0.20	23.0	
20.	Mean rms fluctuational displacement	0.57	1.5	*
21.	Buriedness	0.63	0.8	*
22.	Solvent accessible reduction ratio	0.70	0.4	*
23.	Average number of surrounding residues	0.72	0.4	*
24.	Power to be at the N-terminal of alpha helix	0.57	1.5	*
25.	Power to be at the C-terminal of alpha helix	0.18	26.4	
26.	Power to be at the middle of alpha helix	0.05	38.6	
27.	Partial-specific volume	0.25	18.8	
28.	Average medium-range contacts	0.11	32.7	
29.	Average long-range contacts	0.65	0.7	*
30.	Combined surrounding hydrophobicity (globular and membrane)	0.69	0.4	*
31.	Solvent accessible surface area for denatured protein	0.12	32.7	
32.	Solvent accessible surface area for native protein	0.52	2.5	*
33.	Solvent accessible surface area for protein unfolding	0.47	3.7	*
34.	Gibbs free energy change of hydration for unfolding	0.30	14.1	
35.	Gibbs free energy change of hydration for denatured protein	0.40	7.3	
36.	Gibbs free energy change of hydration for native protein	0.46	4.1	*
37.	Unfolding enthalpy change of hydration	0.05	38.6	
38.	Unfolding entropy change of hydration	0.37	8.9	
39.	Unfolding hydration heat capacity change	0.54	1.9	*
40.	Unfolding Gibbs free energy change of chain	0.16	27.6	
41.	Unfolding enthalpy change of chain	0.22	21.7	
42.	Unfolding entropy change of chain	0.44	4.7	*
43.	Unfolding Gibbs free energy change	0.33	11.0	
44.	Unfolding enthalpy change	0.35	10.2	
45.	Unfolding entropy change	0.34	10.3	
46.	Volume (number of non-hydrogen side chain atoms)	0.11	32.7	
47.	Shape (position of branch point in a side-chain)	0.10	32.8	
48.	Flexibility (number of side-chain dihedral angles)	0.24	19.5	
49.	Backbone dihedral probability	0.51	2.5	*

Conclusion

In this paper, we have proposed a simple method for discriminating 30 folding types of globular proteins. Interestingly, the simplest method is the best method for the truly complicated problems. Although complicated methods

have several possibilities for tuning they generate over fitting to the data set. Further, the method proposed in this work is better than or comparable to other complicated methods, such as, neural networks and support vector machines proposed in the literature for discriminating

folding types. In addition, our method has several advantages including the less computational time and classifying the folds at a single run rather than pair-wise comparisons. We have developed a web server [24], which takes the amino acid sequence as the input and displays the folding type in the output. The main limitation of the method is that its application is restricted to 30 folds considered in this work. However, the approach can be extended to other folds when significant representatives are available.

Methods

Dataset

We have used a dataset of 1612 globular proteins belonging to 30 major folding types obtained from SCOP database [25] for recognizing protein folds. This dataset has been constructed with the following criteria: (i) there should be at least 25 proteins in each fold and (ii) the sequence identity between any two proteins is not more than 25%. The amino acid sequences of all the proteins are available at [24].

Linear discriminant analysis

We have employed LDA in this work and a brief description is given below. First, we compute the amino acid occurrence of each protein,

$$\mathbf{n}_i \equiv (n_{i1}, n_{i2}, \dots, n_{ij}, \dots, n_{i20}),$$

where i is the number of protein; n_{i1}, n_{i2} etc. represents the number of amino acids of each type (Ala, Arg etc.) in i th protein. Then LDA tries to maximize

$$\eta^2 = \frac{S_B}{S_T}.$$

$S_B(S_T)$ is the summation of squared distance between the center of mass of all proteins and that within fold (coordinate of each protein) along axis z , i.e.,

$$S_B \equiv \sum_{k=1}^K N_k (\bar{z} - z_k)^2$$

$$S_T \equiv \sum_i (\bar{z} - z_i)^2,$$

where K is the number of folds, N_k is the number of proteins belonging to k th fold and \bar{z} is the center of mass along the axis z , and z_k is that within k th fold, i.e.,

$$\bar{z} \equiv \frac{1}{N} \sum_i z_i$$

$$z_k \equiv \frac{1}{N_k} \sum_{i'=1}^{N_k} z_{i'},$$

where i' is the i' th protein within the k th fold. z_i is the linear combination of n_{ij} with the set of coefficients $\mathbf{a} \equiv (a_0, a_1, \dots, a_j, \dots, a_{20})$,

$$z_i \equiv a_0 + \sum_j a_j n_{ij}$$

Hence, LDA tries to find \mathbf{a} which maximizes η^2 . In total, we can get 20 kinds of z_i s which are orthogonal to each other, and discrimination is done based on these z_i s. In addition one can introduce weights W_k for each group using the equation:

$$S_B \equiv \sum_{k=1}^K W_k (\bar{z} - z_k)^2 \tag{1}$$

The discrimination is done with Bayesian scheme employing Gaussian kernel. Proteins in each fold are assumed to distribute in amino acid occurrence space obeying Gaussian distribution whose center is the mean occurrence within each fold and variance is computed along the 20 kinds of z coordinates. Then the fold with maximum probability is used assign the folding type of a protein. The probability of each fold may also be used to find other probable folds for a specific sequence.

We have used `lda` module in MASS library of R [26] and the computational time is less than few seconds using Intel Pentium M processor (1.10 GHz) and 1 GB memory.

Scoring

In this paper, we employed four performances to validate the results. We computed TP_k which is the number of proteins being correctly discriminated to be in k th category (e.g., fold). We have also computed FP_k (FN_k), which is the number of proteins which are incorrectly discriminated as being (not being) in k th category. Then we defined sensitivity (or recall), Precision, and F1 as

$$\text{Sensitivity (Recall)} = \frac{TP_k}{TP_k + FN_k}$$

$$\text{Precision} = \frac{TP_k}{TP_k + FP_k}$$

$$F1 = \frac{2 \times \text{Precision} \times \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}}.$$

For validating whole data set we have taken the category average,

$$\frac{1}{K} \sum_{k=1}^K (\text{Performance}),$$

where (Performance) is sensitivity/precision/F1. For some cases denominator of precision and/or F1 will be zero and we excluded these categories to compute the average.

The accuracy is defined as,

$$\text{Accuracy} = \frac{\sum_{k=1}^K TP_k}{N}.$$

N is the total number of proteins.

Availability and requirements

Project name: PROLDA

Project home page: <http://www.granular.com/PROLDA/>

Operating systems : Platform independent

Programing languages : R [26]

Licence: GNU GPL

Any restrictions to use non-academics: none

Authors' contributions

YhT coded the program, carried out most of the calculations and constructed the prediction server. MMG directly supervised the work and provided the dataset of amino acid sequences. All authors contributed in the preparation of the manuscript, read and approved it.

Acknowledgements

This work has been partially supported by the Grant-in-Aid for Creative Scientific Research No.19500254 of the Ministry of Education, Culture, Sports, Science and Technology (MEXT) from 2007 to 2008. We are grateful for their support.

References

- Klein P: **Prediction of protein structural class by discriminant analysis.** *Biochim Biophys Acta* 1986, **874**:205-215.
- Chou KC, Zhang CT: **Diagrammatization of codon usage in 339 human immunodeficiency virus proteins and its biological implication.** *AIDS Res Hum Retroviruses* 1992, **8**:1967-1976.
- Gromiha MM, Ponnuswamy PK: **Prediction of protein secondary structures from their hydrophobic characteristics.** *Int J Pept Protein Res* 1995, **45**:225-240.
- Bu WS, Feng ZP, Zhang Z, Zhang CT: **Prediction of protein (domain) structural classes based on amino-acid index.** *Eur J Biochem* 1999, **266**:1043-1049.
- Wang ZZ, Yuan Z: **How good is prediction of protein structural class by the component-coupled method?** *Proteins* 2000, **38**:165-175.
- Kumarevel TS, Gromiha MM, Ponnuswamy MN: **Structural class prediction: an application of residue distribution along the sequence.** *Biophys Chem* 2000, **88**:81-101.
- Cai YD, Chou KC: **Predicting subcellular localization of proteins in a hybridization space.** *Bioinformatics* 2004, **20**:1151-1156.
- Shen HB, Yang J, Liu XJ, Chou KC: **Using supervised fuzzy clustering to predict protein structural classes.** *Biochem Biophys Res Commun* 2005, **334**:577-581.
- Du QS, Jiang ZQ, He WZ, Li DP, Chou KC: **Amino Acid Principal Component Analysis (AAPCA) and its application in protein structural class prediction.** *J Bio Str Dyn* 2006, **23**:635-640.
- Shi J, Blundell TL, Mizuguchi K: **FUGUE: sequence-structure homology recognition using environment-specific substitution tables and structure-dependent gap penalties.** *J Mol Biol* 2001, **310**:243-257.
- Zhou H, Y Z: **Fold recognition by combining sequence profiles derived from evolution and from depth-dependent structural alignment of fragments.** *Proteins* 2005, **58**:321-328.
- Cheng J, Baldi P: **A machine learning information retrieval approach to protein fold recognition.** *Bioinformatics* 2006, **22**:1456-63.
- Gromiha MM, Suwa M: **A Simple statistical method for discriminating outer membrane proteins with better accuracy.** *Bioinformatics* 2005, **21**:961-968.
- Hirokawa T, Boon-Chieng S, Mitaku S: **SOSUI: classification and secondary structure prediction system for membrane proteins.** *Bioinformatics* 1998, **14**:378-379.
- Chou KC: **Prediction of protein structural classes and subcellular locations.** *Curr Protein Pept Sci* 2000, **1**:171-208.
- Gromiha MM, Selvaraj S, Thangakani AM: **A Statistical method for predicting protein unfolding rates from amino acid sequence.** *J Chem Inf Model* 2006, **46**:1503-1508.
- Gromiha MM, Oobatake M, Kono H, Uedaira H, Sarai A: **Relationship between amino acid properties and protein stability: Buried Mutations.** *J Protein Chem* 1999, **18**:565-578.
- Ding HQD, Dubchak I: **Multi-class protein fold recognition using support vector machines and neural networks.** *Bioinformatics* 2001, **17**:349-358.
- Ofran Y, Margalit H: **Proteins of the same fold and unrelated sequences have similar amino acid composition.** *Proteins* 2006, **64**:275-279.
- Shen HB, Chou KC: **Ensemble classifier for protein fold pattern recognition.** *Bioinformatics* 2006, **22**:1717-1722.
- Gromiha MM, Oobatake M, Sarai A: **Important amino acid properties for enhanced thermostability from mesophilic to thermophilic proteins.** *Biophysical Chemistry* 1999, **82**:51-67.
- Gromiha MM, Oobatake M, Kono H, Uedaira H, Sarai A: **Importance of Mutant Position in Ramachandran Plot for Predicting Protein Stability of Surface Mutations.** *Biopolymers* 2002, **64**:210-220.
- Gromiha MM: **Importance of Native-state Topology for Determining the Folding Rate of Two-state Proteins.** *J Chem Inf Comp Sci* 2003, **43**:1481-1485.
- PROLDA [<http://granular.com/PROLDA/>]
- Murzin AG, Brenner SE, Hubbard T, Chothia C: **SCOP: a structural classification of proteins database for the investigation of sequences and structures.** *J Mol Biol* 1995, **247**:536-540.
- R Development Core Team: **R: A language and environment for statistical computing** 2005 [<http://www.R-project.org>].