Bioinformatics
doi.10.1093/bioinformatics/xxxxxx
Advance Access Publication Date: Day Month Year
Application Note

OXFORD

Structural Bioinformatics

Porter 5: state-of-the-art ab initio prediction of protein secondary structure in 3 and 8 classes

Mirko Torrisi [1,2]*, Manaz Kaleel [1,2] and Gianluca Pollastri [1,2,*]

[1]School of Computer Science and Informatics and
[2]UCD Institute for Discovery.

*To whom correspondence should be addressed.

Associate Editor: XXXXXXX

Received on XXXXX; revised on XXXXX; accepted on XXXXX

Abstract

Motivation: Although Secondary Structure Predictors have been developed for more than 60 years, current ab initio methods have still some way to go to reach their theoretical limits. Moreover, the continuous effort towards harnessing ever increasing data sets and more sophisticated, deeper Machine Learning techniques, has not come to an end.
Results: Here we present Porter 5, the last release of one of the best performing ab initio secondary structure predictor. Version 5 achieves 84% accuracy (84% SOV) when tested on 3 classes, and 73% accuracy (82% SOV) on 8 classes, on a large independent set, significantly outperforming all the most recent ab initio predictors we have tested.
Availability: The web and standalone versions of Porter5 are available at http://distilldeep.ucd.ie/porter.
Contact: name@bio.com
Supplementary information: Supplementary data are available at *Bioinformatics* online.

1 Introduction

The prediction of protein Secondary Structure (SS) has been a central topic of research in Bioinformatics for many decades (Yang *et al.* (2016)). In spite of this, even the most recent and sophisticated ab initio SS predictors are not able to reach the theoretical limit of three-state prediction (88-90%), while only few predictors are currently able to generate eight-state SS predictions.

2 Approach

Similarly to its previous versions (Pollastri and McLysaght (2005)), Porter 5 is based on ensembles of Bidirectional Recurrent Neural Networks (BRNN). Our implementation consists of two similar stages, both of which have a classic BRNN layer followed by a convolutional layer. We have determined the hyperparameters of the system through extensive testing in five-fold cross-validation. The resulting optimal hyperparameters have been used to train the final predictor on the full training set, while the results we report are obtained on a completely independent set. The novel elements of Porter 5 are the use of HHblits (Remmert *et al.* (2012)) in its pipeline alongside PSI-BLAST Schäffer *et al.* (2001), a more informative encoding of the inputs, larger models, deeper training and the reliance on a larger training set than in the previous versions.

3 Methods

3.1 Datasets

The selection, and preparation, of datasets to adopt has a central role in any machine learning method (Walsh *et al.* (2016)). To build the training set we started from the Protein Data Bank (PDB) (Berman *et al.* (2000)) from December 11, 2014, redundancy-reduced it at a 25% sequence identity threshold. For testing purposes we started from the PDB released on June 14, 2017, redundancy-reduced it at a 25% sequence identity threshold against the training set, and then against itself to remove internal redundancy. Finally, all the proteins with at least 10 undetermined amino acids (AA) have been removed from both datasets. The training set contains 15814 proteins and test set 3155 proteins, among the largest ever used to either train or test a SS predictor to the best of our knowledge.

3.2 Alignments

The second key aspect of any SS predictor developed since the early 90's, is harnessing evolutionary information (Rost and Sander (1994)) in the

© The Author 2017. Published by Oxford University Press. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com

form of profiles extracted from multiple sequences. PSI-BLAST (Altschul *et al.* (1997)) has been the reference tool to find remote homologues, and a key component of Porter since its first release (Pollastri and McLysaght (2005)). More recently, HHblits (Remmert *et al.* (2012)) has distinguished itself for fast iterations, and high quality results. Porter 5 relies on both algorithms, iterating them 3 times with an e-value of 0.001. PSI-BLAST is run on the Jun 3, 2016 version of UniRef90 (The UniProt Consortium (2016)). HHblits is run on the February, 2016 version of UniProt20 released by Soeding et. al. Our empirical tests show similar results when a model is trained with either PSI-BLAST or HHblits, but significantly improved results when both are used, either via an ensemble or by concatenating the resulting profiles.

3.3 Encoding

Although the size of the training set is large, our experiments confirm a positive correlation between number of alignments found, and quality of the prediction (Przybylski and Rost (2002)). We do not limit the number of alignment reported by either PSI-BLAST or HHblits, resulting in the generation of alignments with an average of ~12 000, and ~1 200 proteins when PSI-BLAST, and HHblits, respectively. We encode the alignments as frequency profiles. In particular we have 20 frequencies for the standard AA, 1 frequency for unknown or non-standard and one for gaps. Frequencies for AA and gaps are computed separately, that is: AA frequencies are computed ignoring gaps, while the gap frequency is equal to the total number of gaps divided by the total number of sequences aligned. Aligned sequences are weighed by the information they carry with respect to the unweighed frequency profile (Krogh and Mitchison (1995))), which in our test results in a small performance improvement. Moreover, the frequency for the AA appearing in the query sequence is artificially "clipped" to 1. This does not reduce the information of the profile, any one of the values in the initial (unclipped) profile is equal to 1 minus the sum of the others, while encoding into the input the identity of the query sequence. We have found this simple trick to be very beneficial in our tests, leading to significant performance improvements. We also build a version of the predictor which outputs the 8 SS classes produced by the DSSP program Kabsch and Sander (1983). In this case three more numbers, representing the output of the three-state Porter 5, are added to the input.

3.4 Model and Training

We conducted a preliminary training phase to identify optimal hyperparameters using only the training set in 5-fold cross-validation. As a passing note, we extensively tested many types of neural network, including convolutional networks of increasing depths and simple windowed neural networks with up to 17 hidden layers, but our two-stage BRNN model (Pollastri and McLysaght (2005)) performed over 1% better than any of the alternatives we tried. The hyperparameters selected for the BRNNs trained on PSI-BLAST appeared close to optimal for both the BRNN trained on HHblits, and the BRNN trained on the concatenation of the inputs created with HHblits and PSI-BLAST. Only minor tweaking of the hyperparameters were needed when switching between three-state and eight-state SS. Purely based on the training set we settled on an ensemble of 7 BRNN: 3 trained on PSI-BLAST, 3 trained on HHblits, and 1 trained on both (44 concatenated inputs rather than 22). These 7 BRNN were then trained on the full training set (on either three-state, or eight-state targets). The relatively small scale of the ensemble and the modest size of the individual models (on average 39k free parameters for the 3-class networks, 58k for 8 classes) ensure high speed during prediction time without affecting the accuracy or SOV score (Table 1). The test set was only used at the final stage, to obtain unbiased performance estimates for Porter 5 and other recent SS predictors (Walsh *et al.* (2016)).

4 Results

We tested Porter 5 against Porter 4 Mirabello and Pollastri (2013), SPIDER3 Heffernan *et al.* (2017), SSpro 5 Baldi *et al.* (1999), PSIPRED 4.01 (Jones (1999)), RaptorX-PropertyWang *et al.* (2016b) and DeepCNF-SS (Wang *et al.* (2016a)) on the test set we created, containing 3155 proteins. However we were limited in this by the fact that SPIDER3 rejects proteins containing undetermined (X) amino acids (911 in the test set contain at least one), and that when we use the parameters required by SPIDER3, either PSI-BLAST or HHblits do not return a valid result for 40 proteins. Because of this we report performance results on two sets: one where we exclude the proteins on which we could not obtain a valid response from SPIDER3, containing 2204 entries in total (Table 1); the full set of 3155 proteins (Table 2) on which SPIDER3 is not assessed.

Porter 5 is the most accurate predictor in our tests with 3-class accuracy just shy of 84% on the smaller testing set and 84.2% on the larger set, 0.7% better than SPIDER3, 1.2% and 1.6% better than SSpro with templates, and 2% more accurate than all the other predictors. Porter 5 is also very fast compared to the alternatives given the relatively small size of its models and the fact that it is built on in-house, heavily profiled code. For instance, once the alignments by PSI-BLAST and HHblits are present, Porter 5.0 runs 2 orders of magnitude faster than SPIDER3, although SPIDER3 is able to predict backbone angles, contact numbers, and solvent accessibility at the same time as secondary structure. Thus, to fully exploit its speed, we assess and make available a version of Porter 5 which is roughly three times faster depending on HHblits only. SPIDER3 is also the only SS predictor analyzed - except Porter 5 - that generates three-state predictions with an average Q3 accuracy greater than 83% (Table 1).

Table 1. Q3 accuracy and SOV score on 2204 proteins.

Method	Q3 per AA	SOV per AA	Q3 per protein	SOV per protein
Porter 5	**83.89%**	**83.32%**	**84.32%**	**84.53%**
SPIDER3	83.18%	82.06%	83.39%	83.15%
Porter 5 (HHblits only)	83.13%	82.27%	83.67%	83.63%
SSpro 5 with templates	82.65%	80.13%	83.91%	82.42%
RaptorX-Property	81.97%	81.99%	82.59%	83.15%
PSIPRED 4.01	81.93%	80.09%	82.47%	81.57%
Porter 4	81.72%	81.13%	82.27%	82.43%
SSpro 5 ab initio	81.67%	78.94%	81.50%	79.74%
DeepCNF	81.11%	80.86%	81.18%	81.44%

Performances on the set for which SPIDER3 generates predictions, sorted by Q3 accuracy.

The test set has been reduced only against our training set, so our assessment of other recent SS predictors might be somewhat optimistic. However, Porter 5 is the best three-states and eight-states SS predictor according to all the measures observed on this test set. Porter 5 with HHblits only performs better than SSpro 5 with templates and is at least comparable to SPIDER3.

We have also analysed the performance of Porter 5 separately on proteins resolved by Nuclear Magnetic Resonance (NMR) and by X-ray crystallography. NMR proteins are predicted at a significantly lower Q3 (81.6%), possibly because of their different statistics (e.g. average length and composition) or less certain determination of SS. The X-ray only section of the test set, which is roughly 90% of the total, is predicted at an average Q3 of 84.65% (Table 3).

Table 2. Q3/Q8 accuracy and SOV score on the full test set

Method	Q3	SOV	Q8	SOV
Porter 5	**84.19%**	**83.99%**	**73.02%**	**76.83%**
Porter 5 (HHblits only)	83.39%	82.86%	71.80%	75.45%
SSpro 5 with templates	82.62%	80.65%	71.91%	78.55%
PSIPRED 4.01	82.06%	80.55%	N.A.	N.A.
RaptorX-Property	82.04%	82.30%	70.74%	74.88%
Porter 4	82.00%	81.85%	N.A.	N.A.
DeepCNF	81.00%	81.02%	69.76%	73.60%
SSpro 5 ab initio	80.70%	78.68%	68.85%	72.26%

Table 3. Porter 5 assesed on NMR vs X-ray crystallography

	Q3	SOV	Q8	SOV
NMR	81.61%	78.23%	67.52%	70.71%
X-ray	**84.65%**	**85.08%**	**74%**	**77.93%**

5 Conclusion

We have built a state-of-the-art 3- and 8-state predictor of protein SS, Porter 5. In our tests it improves by roughly 2% accuracy on its previous version, and outperforms all the most recent predictors of secondary structure, included a template based one. Porter is freely available as a web server at http://distilldeep.ucd.ie/porter and also as a standalone program at the same address, alongside with all the datasets, and alignments generated.

Acknowledgements

We acknowledge the key role of the UCD cluster, and the UCD Research IT staff.

Funding

The work of M.T., and M.K. is supported by the Irish Research Council [GOIPG/2015/3717, and GOIPG/2014/603].

References

Altschul, S. F., Madden, T. L., Schäffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research*, **25**(17), 3389–3402.

Baldi, P., Brunak, S., Frasconi, P., Soda, G., and Pollastri, G. (1999). Exploiting the past and the future in protein secondary structure prediction. *Bioinformatics (Oxford, England)*, **15**(11), 937–946.

Berman, H. M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T. N., Weissig, H., Shindyalov, I. N., and Bourne, P. E. (2000). The Protein Data Bank. *Nucleic Acids Research*, **28**(1), 235–242.

Heffernan, R., Yang, Y., Paliwal, K., and Zhou, Y. (2017). Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. *Bioinformatics*, **33**(18), 2842–2849.

Jones, D. T. (1999). Protein secondary structure prediction based on position-specific scoring matrices. *Journal of Molecular Biology*, **292**(2), 195–202.

Kabsch, W. and Sander, C. (1983). Dictionary of protein secondary structure: Pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers*, **22**(12), 2577–2637.

Krogh, A. and Mitchison, G. (1995). Maximum entropy weighting of aligned sequences of proteins or DNA. *Proceedings. International Conference on Intelligent Systems for Molecular Biology*, **3**, 215–221.

Mirabello, C. and Pollastri, G. (2013). Porter, PaleAle 4.0: high-accuracy prediction of protein secondary structure and relative solvent accessibility. *Bioinformatics*, **29**(16), 2056–2058.

Pollastri, G. and McLysaght, A. (2005). Porter: a new, accurate server for protein secondary structure prediction. *Bioinformatics*, **21**(8), 1719–1720.

Przybylski, D. and Rost, B. (2002). Alignments grow, secondary structure prediction improves. *Proteins*, **46**(2), 197–205.

Remmert, M., Biegert, A., Hauser, A., and Söding, J. (2012). HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. *Nature Methods*, **9**(2), 173–175.

Rost, B. and Sander, C. (1994). Combining evolutionary information and neural networks to predict protein secondary structure. *Proteins: Structure, Function, and Bioinformatics*, **19**(1), 55–72.

Schäffer, A. A., Aravind, L., Madden, T. L., Shavirin, S., Spouge, J. L., Wolf, Y. I., Koonin, E. V., and Altschul, S. F. (2001). Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements. *Nucleic Acids Research*, **29**(14), 2994–3005.

The UniProt Consortium (2016). UniProt: the universal protein knowledgebase. *Nucleic Acids Research*, **45**(D1), D158–D169.

Walsh, I., Pollastri, G., and Tosatto, S. C. E. (2016). Correct machine learning on protein sequences: a peer-reviewing perspective. *Briefings in Bioinformatics*, **17**(5), 831–840.

Wang, S., Peng, J., Ma, J., and Xu, J. (2016a). Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields. *Scientific Reports*, **6**.

Wang, S., Li, W., Liu, S., and Xu, J. (2016b). RaptorX-Property: a web server for protein structure property prediction. *Nucleic Acids Research*, **44**(W1), W430–W435.

Yang, Y., Gao, J., Wang, J., Heffernan, R., Hanson, J., Paliwal, K., and Zhou, Y. (2016). Sixty-five years of the long march in protein secondary structure prediction: the final stretch? *Briefings in Bioinformatics*.