References

[1]   Y. Yang, J. Gao, J. Wang, R. Heffernan, J. Hanson, K. Paliwal, Y. Zhou, Sixty-five years of the long march in protein secondary structure prediction: The final stretch?, Brief. Bioinform. (2018). https://doi.org/10.1093/bib/bbw129.

[2]   C.A. Hunter, Sequence-dependent DNA structure the role of base stacking interactions, J. Mol. Biol. 230 (1993) 1025–1054. https://doi.org/10.1006/jmbi.1993.1217.

[3]   M.J. Zvelebil, G.J. Barton, W.R. Taylor, M.J.E. Sternberg, Prediction of protein secondary structure and active sites using the alignment of homologous sequences, J. Mol. Biol. 195 (1987) 957–961. https://doi.org/10.1016/0022-2836(87)90501-8.

[4]   R. Heffernan, K. Paliwal, J. Lyons, J. Singh, Y. Yang, Y. Zhou, Single-sequence-based prediction of protein secondary structures and solvent accessibility by deep whole-sequence learning, J. Comput. Chem. 39 (2018) 2210–2216. https://doi.org/10.1002/jcc.25534.

[5]   R. Heffernan, K. Paliwal, J. Lyons, A. Dehzangi, A. Sharma, J. Wang, A. Sattar, Y. Yang, Y. Zhou, Improving prediction of secondary structure, local backbone angles, and solvent accessible surface area of proteins by iterative deep learning, Sci. Rep. 5 (2015) 1–11. https://doi.org/10.1038/srep11476.

[6]   R. Heffernan, Y. Yang, K. Paliwal, Y. Zhou, 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 (2017) 2842–2849. https://doi.org/10.1093/bioinformatics/btx218.

[7]   Y. Wang, H. Mao, Z. Yi, Protein secondary structure prediction by using deep learning method, Knowledge-Based Syst. 118 (2017) 115–123. https://doi.org/10.1016/j.knosys.2016.11.015.

[8]   M.N. Faraggi, A. Arnau, V.M. Silkin, Role of band structure and local-field effects in the low-energy collective electronic excitation spectra of 2H-NbSe 2, Phys. Rev. B - Condens. Matter Mater. Phys. 86 (2012) 035115. https://doi.org/10.1103/PhysRevB.86.035115.

[9]   J. Chung, C. Gulcehre, K. Cho, Empirical Evaluation of Gated Recurrent Neural Networks on Sequence Modeling, n.d.

[10]   Y. Yang, J. Gao, J. Wang, R. Heffernan, J. Hanson, K. Paliwal, Y. Zhou, Sixty-five years of the long march in protein secondary structure prediction: The final stretch?, Brief. Bioinform. 19 (2018) 482–494. https://doi.org/10.1093/bib/bbw129.

[11]   D. Li, T. Li, P. Cong, W. Xiong, J. Sun, A novel structural position-specific scoring matrix for the prediction of protein secondary structures, 28 (2012) 32–39. https://doi.org/10.1093/bioinformatics/btr611.

[12] Q. Jiang, X. Jin, S.-J. Lee, S. Yao, Protein secondary structure prediction: A survey of the state of the art., J. Mol. Graph. Model. 76 (2017) 379–402. https://doi.org/10.1016/j.jmgm.2017.07.015.

[13] J. Zhou, H. Wang, Z. Zhao, R. Xu, Q. Lu, CNNH_PSS: Protein 8-class secondary structure prediction by convolutional neural network with highway, BMC Bioinformatics. 19 (2018). https://doi.org/10.1186/s12859-018-2067-8.

[14] A. Drozdetskiy, C. Cole, J. Procter, G.J. Barton, JPred4: a protein secondary structure prediction server, Nucleic Acids Res. 43 (2015) W389–W394. https://doi.org/10.1093/nar/gkv332.

[15] Y. Wang, H. Mao, Z. Yi, Protein secondary structure prediction by using deep learning method, Knowledge-Based Syst. (2017). https://doi.org/10.1016/j.knosys.2016.11.015.

[16] M.D. Yandell, W.H. Majoros, Genomics and natural language processing, Nat. Rev. Genet. 3 (2002) 601–610. https://doi.org/10.1038/nrg861.

[17] K. Motomura, T. Fujita, M. Tsutsumi, S. Kikuzato, M. Nakamura, J.M. Otaki, Word Decoding of Protein Amino Acid Sequences with Availability Analysis: A Linguistic Approach, PLoS One. 7 (2012). https://doi.org/10.1371/journal.pone.0050039.

[18] D.B. Searls, The language of genes, Nature. 420 (2002) 211–217. https://doi.org/10.1038/nature01255.

[19] J.C. Kendrew, G. Bodo, H.M. Dintzis, R.G. Parrish, H. Wyckoff, D.C. Phillips, A three-dimensional model of the myoglobin molecule obtained by x-ray analysis, Nature. (1958). https://doi.org/10.1038/181662a0.

[20] N.E. Hafsa, D. Arndt, D.S. Wishart, CSI 3.0: a web server for identifying secondary and super-secondary structure in proteins using NMR chemical shifts., Nucleic Acids Res. 43 (2015) W370-7. https://doi.org/10.1093/nar/gkv494.

[21] A. Dong, P. Huang, W.S. Caughey, Protein Secondary Structures in Water from Second-Derivative Amide I Infrared Spectra, Biochemistry. (1990). https://doi.org/10.1021/bi00465a022.

[22] H.K. Ho, L. Zhang, K. Ramamohanarao, S. Martin, A survey of machine learning methods for secondary and supersecondary protein structure prediction., Methods Mol. Biol. 932 (2013) 87–106. https://doi.org/10.1007/978-1-62703-065-6_6.

[23] P.Y. Chou, G.D. Fasman, Prediction of Protein Conformation, Biochemistry. (1974). https://doi.org/10.1021/bi00699a002.

[24] A. V. Finkelstein, O.B. Ptitsyn, Statistical analysis of the correlation among amino acid residues in helical, β-stractural and non-regular regions of globular proteins, J. Mol. Biol. (1971). https://doi.org/10.1016/0022-2836(71)90160-4.

[25] S. Hua, Z. Sun, A novel method of protein secondary structure prediction with

high segment overlap measure: support vector machine approach., J. Mol. Biol. 308 (2001) 397–407. https://doi.org/10.1006/jmbi.2001.4580.

[26]   S. Wang, J. Peng, J. Ma, J. Xu, Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields, Sci. Rep. 6 (2016). https://doi.org/10.1038/srep18962.

[27]   Y. Guo, B. Wang, W. Li, B. Yang, Protein secondary structure prediction improved by recurrent neural networks integrated with two-dimensional convolutional neural networks, J. Bioinform. Comput. Biol. 16 (2018) 1850021. https://doi.org/10.1142/S021972001850021X.

[28]   G. Hinton, L. Deng, D. Yu, G. Dahl, A.-R. Mohamed, N. Jaitly, A. Senior, V. Vanhoucke, P. Nguyen, T. Sainath, B. Kingsbury, Deep Neural Networks for Acoustic Modeling in Speech Recognition, n.d.

[29]   K. He, X. Zhang, S. Ren, J. Sun, Deep Residual Learning for Image Recognition, n.d. http://image-net.org/challenges/LSVRC/2015/.

[30]   C. Nogueira, D. Santos, M. Gatti, Deep Convolutional Neural Networks for Sentiment Analysis of Short Texts, n.d.

[31]   B. Zhang, J. Li, Q. Lü, Prediction of 8-state protein secondary structures by a novel deep learning architecture, BMC Bioinformatics. (2018). https://doi.org/10.1186/s12859-018-2280-5.

[32]   Z. Li, Y. Yu, Protein Secondary Structure Prediction Using Cascaded Convolutional and Recurrent Neural Networks, n.d. http://www.rcsb.org/pdb/explore/explore.do?structureId=154L.

[33]   G. Pollastri, D. Przybylski, B. Rost, P. Baldi, Improving the prediction of protein secondary structure in three and eight classes using recurrent neural networks and profiles, Proteins Struct. Funct. Genet. 47 (2002) 228–235. https://doi.org/10.1002/prot.10082.

[34]   S.K. Sønderby, O. Winther, Protein Secondary Structure Prediction with Long Short Term Memory Networks, (2014). http://arxiv.org/abs/1412.7828 (accessed January 15, 2020).

[35]   J. Zhou, O.G. Troyanskaya, Deep Supervised and Convolutional Generative Stochastic Network for Protein Secondary Structure Prediction, n.d.

[36]   C.N. Magnan, P. Baldi, SSpro/ACCpro 5: Almost perfect prediction of protein secondary structure and relative solvent accessibility using profiles, machine learning and structural similarity, Bioinformatics. 30 (2014) 2592–2597. https://doi.org/10.1093/bioinformatics/btu352.

[37]   Y. Bengio, P. Simard, P. Frasconi, Learning Long-Term Dependencies with Gradient Descent is Difficult, IEEE Trans. Neural Networks. (1994). https://doi.org/10.1109/72.279181.

[38]   S. Hochreiter, A.S. Younger, P.R. Conwell, Learning to learn using gradient descent, in: Lect. Notes Comput. Sci. (Including Subser. Lect. Notes Artif.

Intell. Lect. Notes Bioinformatics), 2001. https://doi.org/10.1007/3-540-44668-0_13.

[39] S. Hochreiter, J. Schmidhuber, Long Short-Term Memory, Neural Comput. (1997). https://doi.org/10.1162/neco.1997.9.8.1735.

[40] G.E. Hinton, Connectionist learning procedures, Artif. Intell. 40 (1989) 185–234. https://doi.org/10.1016/0004-3702(89)90049-0.

[41] T. Mikolov, K. Chen, G. Corrado, J. Dean, Distributed Representations of Words and Phrases and their Compositionality, 2013.

[42] RCSB PDB: Homepage, (n.d.). https://www.rcsb.org/ (accessed April 17, 2020).

[43] G. Wang, R.L. Dunbrack, PISCES: a protein sequence culling server, Bioinforma. Appl. NOTE. 19 (2003) 1589–1591. https://doi.org/10.1093/bioinformatics/btg224.

[44] B. Rost, C. Sander, Improved prediction of protein secondary structure by use of sequence profiles and neural networks., Proc. Natl. Acad. Sci. U. S. A. 90 (1993) 7558–62. https://doi.org/10.1073/pnas.90.16.7558.

[45] W. Kabsch, C. Sander, Dictionary of protein secondary structure: Pattern recognition of hydrogen-bonded and geometrical features, Biopolymers. (1983). https://doi.org/10.1002/bip.360221211.

[46] M. Schuster, K.K. Paliwal, Bidirectional recurrent neural networks, IEEE Trans. Signal Process. 45 (1997) 2673–2681. https://doi.org/10.1109/78.650093.

[47] Home - Keras Documentation, (n.d.). https://keras.io/ (accessed January 15, 2020).

[48] TensorFlow White Papers | TensorFlow, (n.d.). https://www.tensorflow.org/about/bib (accessed January 15, 2020).

[49] G. Hinton, N. Srivastava, K. Swersky, Neural Networks for Machine Learning Lecture 6a Overview of mini---batch gradient descent, n.d.

[50] Z. Aydin, Y. Altunbasak, M. Borodovsky, Protein secondary structure prediction for a single-sequence using hidden semi-Markov models, BMC Bioinformatics. 7 (2006). https://doi.org/10.1186/1471-2105-7-178.

[51] M.S. Patel, H.S. Mazumdar, Knowledge base and neural network approach for protein secondary structure prediction, J. Theor. Biol. 361 (2014) 182–189. https://doi.org/10.1016/j.jtbi.2014.08.005.

[52] K. Lin, V.A. Simossis, W.R. Taylor, J. Heringa, A simple and fast secondary structure prediction method using hidden neural networks, Bioinforma. Orig. Pap. 21 (2005) 152–159. https://doi.org/10.1093/bioinformatics/bth487.

[53] B. Rost, C. Sander, R. Schneider, PHD-an automatic mail server for protein secondary structure prediction, Bioinformatics. 10 (1994) 53–60.

https://doi.org/10.1093/bioinformatics/10.1.53.

[54]   M. Ashburner, A.P. Davis, J.E. Richardson, S. Lewis, D. Botstein, J.C. Matese, H. Butler, C.A. Ball, L. Issel-Tarver, K. Dolinski, G. Sherlock, D.P. Hill, M.A. Harris, M. Ringwald, S.S. Dwight, A. Kasarskis, J.M. Cherry, J.A. Blake, G.M. Rubin, J.T. Eppig, Gene Ontology: tool for the unification of biology, Nat. Genet. (2002). https://doi.org/10.1038/75556.

[55]   C. Cole, J.D. Barber, G.J. Barton, The Jpred 3 secondary structure prediction server., Nucleic Acids Res. 36 (2008) 197–201. https://doi.org/10.1093/nar/gkn238.

[56]   P. Yoo, B. Zhou, A. Zomaya, Machine Learning Techniques for Protein Secondary Structure Prediction:An Overview and Evaluation, Curr. Bioinform. (2008). https://doi.org/10.2174/157489308784340676.

[57]   A. Kloczkowski, K.L. Ting, R.L. Jernigan, J. Garnier, Combining the GOR V algorithm with evolutionary information for protein secondary structure prediction from amino acid sequence, Proteins Struct. Funct. Genet. 49 (2002) 154–166. https://doi.org/10.1002/prot.10181.

[58]   B. Liu, F. Liu, X. Wang, J. Chen, L. Fang, K.-C. Chou, Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences, Nucleic Acids Res. 43 (2015) 65–71. https://doi.org/10.1093/nar/gkv458.

[59]   B. Liu, X. Gao, H. Zhang, BioSeq-Analysis2.0: an updated platform for analyzing DNA, RNA and protein sequences at sequence level and residue level based on machine learning approaches, Nucleic Acids Res. 47 (2019). https://doi.org/10.1093/nar/gkz740.

[60]   B. Liu, H. Wu, D. Zhang, X. Wang, K.-C. Chou, Pse-Analysis: a python package for DNA/RNA and protein/ peptide sequence analysis based on pseudo components and kernel methods, Oncotarget. 8 (2017) 13338–13343. https://doi.org/10.1093/bioinformatics/btw539.

[61]   Z. Chen, P. Zhao, F. Li, A. Leier, T.T. Marquez-Lago, Y. Wang, G.I. Webb, A.I. Smith, R.J. Daly, K.-C. Chou, J. Song, iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences, Bioinformatics. 34 (2018) 2499–2502. https://doi.org/10.1093/bioinformatics/bty140.

[62]   A. Busia, J. Collins, N. Jaitly, Protein Secondary Structure Prediction Using Deep Multi-scale Convolutional Neural Networks and Next-Step Conditioning, n.d. http://www.princeton.edu/ (accessed January 15, 2020).

[63]   Z. Lin, J. Lanchantin, Y. Qi, MUST-CNN: A Multilayer Shift-and-Stitch Deep Convolutional Architecture for Sequence-Based Protein Structure Prediction, n.d. www.aaai.org (accessed January 15, 2020).

[64]   G. Pollastri, D. Przybylski, B. Rost, P. Baldi, Improving the prediction of protein secondary structure in three and eight classes using recurrent neural

networks and profiles., Proteins. 47 (2002) 228–35. http://www.ncbi.nlm.nih.gov/pubmed/11933069 (accessed August 1, 2019).

[65] Z. Li, Y. Yu, Protein secondary structure prediction using cascaded convolutional and recurrent neural networks, IJCAI Int. Jt. Conf. Artif. Intell. 2016-Janua (2016) 2560–2567.

[66] M.-T. Luong, R. Socher, C.D. Manning, Better Word Representations with Recursive Neural Networks for Morphology, n.d. http://nlp.stanford.edu/ (accessed January 19, 2021).

[67] W. Ling, I. Trancoso, C. Dyer, A.W. Black, Character-based Neural Machine Translation, (2015). http://arxiv.org/abs/1511.04586 (accessed January 8, 2021).

[68] C. Dyer, M. Ballesteros, W. Ling, A. Matthews, N.A. Smith, Transition-Based Dependency Parsing with Stack Long Short-Term Memory, ACL-IJCNLP 2015 - 53rd Annu. Meet. Assoc. Comput. Linguist. 7th Int. Jt. Conf. Nat. Lang. Process. Asian Fed. Nat. Lang. Process. Proc. Conf. 1 (2015) 334–343. http://arxiv.org/abs/1505.08075 (accessed January 19, 2021).

[69] C.N. dos Santos, V. Guimarães, Boosting Named Entity Recognition with Neural Character Embeddings, (2015) 25–33. http://arxiv.org/abs/1505.05008 (accessed January 19, 2021).

[70] J. Chung, S. Ahn, Y. Bengio, Hierarchical Multiscale Recurrent Neural Networks, (2016). http://arxiv.org/abs/1609.01704 (accessed January 19, 2021).

[71] K. Evang, V. Basile, G. Chrupala, J. Bos, Elephant: Sequence Labeling for Word and Sentence Segmentation, 2013. https://hal.archives-ouvertes.fr/hal-01344500 (accessed January 19, 2021).

[72] G. Chrupała, Text segmentation with character-level text embeddings, (2013). http://arxiv.org/abs/1309.4628 (accessed January 19, 2021).

[73] Y. Kim, P.R. Moorcroft, I. Aleinov, M.J. Puma, N.Y. Kiang, Variability of phenology and fluxes of water and carbon with observed and simulated soil moisture in the Ent Terrestrial Biosphere Model (Ent TBM version 1.0.1.0.0), Geosci. Model Dev. 8 (2015) 3837–3865. https://doi.org/10.5194/gmd-8-3837-2015.

[74] C. Nogueira, D. Santos, B. Zadrozny, Learning Character-level Representations for Part-of-Speech Tagging, PMLR, 2014. http://proceedings.mlr.press/v32/santos14.html (accessed January 19, 2021).

[75] J. Moult, K. Fidelis, A. Kryshtafovych, A. Tramontano, Critical assessment of methods of protein structure prediction (CASP)-round IX, Proteins Struct. Funct. Bioinforma. 79 (2011) 1–5. https://doi.org/10.1002/prot.23200.

[76] M. Schuster, K.K. Paliwal, Bidirectional recurrent neural networks, IEEE Trans. Signal Process. (1997). https://doi.org/10.1109/78.650093.

[77] S. Wang, W. Li, S. Liu, J. Xu, RaptorX-Property: a web server for protein structure property prediction, Nucleic Acids Res. 44 (2016) W430–W435. https://doi.org/10.1093/nar/gkw306.

[78] C. Fang, Y. Shang, D. Xu, MUFOLD-SS: New Deep Inception-Inside-Inception Networks for Protein Secondary Structure Prediction, (n.d.). https://doi.org/10.1002/prot.25487.

[79] H. Hu, Z. Li, A. Elofsson, S. Xie, A Bi-LSTM Based Ensemble Algorithm for Prediction of Protein Secondary Structure, Appl. Sci. 9 (2019) 3538. https://doi.org/10.3390/app9173538.

[80] A. Drozdetskiy, C. Cole, J. Procter, G.J. Barton, JPred4: A protein secondary structure prediction server, Nucleic Acids Res. 43 (2015) W389–W394. https://doi.org/10.1093/nar/gkv332.

[81] Z. Wang, F. Zhao, J. Peng, J. Xu, Protein 8-class secondary structure prediction using conditional neural fields., Proteomics. 11 (2011) 3786–92. https://doi.org/10.1002/pmic.201100196.

[82] I. Sutskever, O. Vinyals, Q. V. Le, Sequence to Sequence Learning with Neural Networks, Adv. Neural Inf. Process. Syst. 4 (2014) 3104–3112. http://arxiv.org/abs/1409.3215 (accessed January 8, 2021).

[83] Y. Lepage, E. Denoual, ALEPH: an EBMT system based on the preservation of proportional analogies between sentences across languages, n.d. http://www.isca-speech.org/archive (accessed January 8, 2021).

[84] J. Tiedemann, P. Nakov, Analyzing the Use of Character-Level Translation with Sparse and Noisy Datasets, 2013.

[85] D. Vilar, J. Xu, L.F. D'Haro, H. Ney, Error Analysis of Statistical Machine Translation Output, (2006). http://www.lrec-conf.org/proceedings/lrec2006/pdf/413_pdf.pdf (accessed January 8, 2021).

[86] M.R. Costa-Jussà, J.A.R. Fonollosa, Character-based neural machine translation, in: 54th Annu. Meet. Assoc. Comput. Linguist. ACL 2016 - Short Pap., Association for Computational Linguistics (ACL), 2016: pp. 357–361. https://doi.org/10.18653/v1/p16-2058.

[87] M.-T. Luong, H. Pham, C.D. Manning, Effective Approaches to Attention-based Neural Machine Translation, (2015). https://arxiv.org/abs/1508.04025v5 (accessed January 8, 2021).

[88] R. Sennrich, B. Haddow, A. Birch, Neural Machine Translation of Rare Words with Subword Units, (2015). https://arxiv.org/abs/1508.07909v5 (accessed January 8, 2021).

[89] E. Vylomova, T. Cohn, X. He, G. Haffari, Word Representation Models for Morphologically Rich Languages in Neural Machine Translation, in: Proc. First Work. Subword Character Lev. Model. NLP, Association for Computational Linguistics (ACL), 2018: pp. 103–108. https://doi.org/10.18653/v1/w17-4115.

[90] A. Drozdetskiy, C. Cole, J. Procter, G.J. Barton, JPred4: A protein secondary structure prediction server, Nucleic Acids Res. (2015). https://doi.org/10.1093/nar/gkv332.

[91] D. Ganguly, D. Roy, M. Mitra, G.J.F. Jones, Word Embedding based Generalized Language Model for Information Retrieval, in: 2015. https://doi.org/10.1145/2766462.2767780.

[92] M. Ashburner, C.A. Ball, J.A. Blake, D. Botstein, H. Butler, J.M. Cherry, A.P. Davis, K. Dolinski, S.S. Dwight, J.T. Eppig, M.A. Harris, D.P. Hill, L. Issel-Tarver, A. Kasarskis, S. Lewis, J.C. Matese, J.E. Richardson, M. Ringwald, G.M. Rubin, G. Sherlock, Gene ontology: Tool for the unification of biology, Nat. Genet. (2000). https://doi.org/10.1038/75556.

[93] J. Chen, G. Liu, V. Pantalone, Q. Zhong, Physicochemical properties of proteins extracted from four new Tennessee soybean lines, J. Agric. Food Res. 2 (2020) 100022. https://doi.org/10.1016/j.jafr.2020.100022.

[94] C. Mirabello, G. Pollastri, Porter, PaleAle 4.0: High-accuracy prediction of protein secondary structure and relative solvent accessibility, Bioinformatics. 29 (2013) 2056–2058. https://doi.org/10.1093/bioinformatics/btt344.

[95] A. Yaseen, Y. Li, Context-based features enhance protein secondary structure prediction accuracy, J. Chem. Inf. Model. 54 (2014) 992–1002. https://doi.org/10.1021/ci400647u.

[96] L.J. McGuffin, K. Bryson, D.T. Jones, The PSIPRED protein structure prediction server, Bioinformatics. 16 (2000) 404–405. https://doi.org/10.1093/bioinformatics/16.4.404.

[97] R.D. Finn, J. Clements, S.R. Eddy, HMMER web server: Interactive sequence similarity searching, Nucleic Acids Res. 39 (2011) W29. https://doi.org/10.1093/nar/gkr367.

[98] S. Wang, J. Peng, J. Ma, J. Xu, Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields, Sci. Rep. (2016). https://doi.org/10.1038/srep18962.

[99] Y. Ma, Y. Liu, J. Cheng, Protein secondary structure prediction based on data partition and semi-random subspace method, Sci. Rep. 8 (2018). https://doi.org/10.1038/s41598-018-28084-8.

[100] D. Wei, Q. Jiang, Y. Wei, S. Wang, A novel hierarchical clustering algorithm for gene sequences, BMC Bioinformatics. 13 (2012) 174. https://doi.org/10.1186/1471-2105-13-174.

[101] J. Pennington, R. Socher, C.D. Manning, GloVe: Global Vectors for Word Representation, (n.d.). http://nlp. (accessed August 26, 2021).

[102] A. Joulin, E. Grave, P. Bojanowski, M. Douze, H. Jégou, T. Mikolov, FastText.zip: Compressing text classification models, (2016). https://arxiv.org/abs/1612.03651v1 (accessed August 26, 2021).

[103] Chris McCormick · Machine Learning Tutorials and Insights, (n.d.). http://mccormickml.com/ (accessed August 26, 2021).

[104] Y. Yang, J. Gao, J. Wang, R. Heffernan, J. Hanson, K. Paliwal, Y. Zhou, Sixty-five years of the long march in protein secondary structure prediction: The final stretch?, Brief. Bioinform. 19 (2018) 482–494. doi:10.1093/bib/bbw129.

[105] H. Deng, Y. Jia, Y. Zhang, Protein structure prediction, Int. J. Mod. Physics. B. 32 (2018). doi:10.1142/S021797921840009X.

List of Papers Published /Communicated

List of papers published/ accepted in journals:

Published:

1. Ashish Kumar Sharma and Rajeev Srivastava, "Protein Secondary Structure Prediction using Character n-gram Embedding and Bi-LSTM", Current Bioinformatics (2020) 15:1.

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2. Ashish Kumar Sharma and Rajeev Srivastava, "Variable Length Character N-Gram Embedding of Protein Sequences for Secondary Structure Prediction", Protein & Peptide Letters (2020) 27: 1.

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