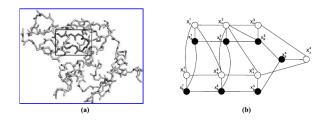Inria Sophia Antipolis
Group: Algorithms-Biology-Structure
Frederic.Cazals@inria.fr
Web: http://team.inria.fr/abs

MASTER INTERNSHIP PROPOSAL

Figure 1: Protein structure in which the spatial proximity between amino acids is encoded using a graphical model. From [1].

ATTENTION MECHANISMS FOR GRAPHICAL MODELS, WITH APPLICATIONS TO PROTEIN STRUCTURE ANALYSIS.

Keywords: deep learning, attention mechanisms, transformers, message passing, belief propagation, enumeration, approximation algorithms, free energy, protein structure analysis.

Context. Emerging from the field of natural language processing, (self-)attention mechanisms have proven essential to understand the coupling between tokens in a sentence [2, 3]. In a different context, graphical models make it possible to express the conditional dependence of random variables encoded in graph nodes via the edges of the graph. On such models, message passing algorithms provide effective ways to compute various quantities of interest, in particular partition functions and free energies [4, 5].

Recently, attention mechanisms have also proven key to encode the coupling between spatial patterns observed between amino acids in a protein structure [6]. The corresponding tool, `AlphaFold` by Deepmind, is considered a major achievement to predict a plausible structure of a protein from its amino-acid sequence. In related work, message passing algorithms have been used to compute average properties of proteins [1].

Goals. `AlphaFold` is a key achievement but outputs a single structure. In fact, statistical physics teaches us that observable properties of molecules depend on ensemble of conformations (weighted by Boltzmann'f factor). (See also AI, molecular design and the Covid19.)

The goal of this internship will be to extend attention mechanisms in the context of graphical models, to study ensembles of conformations rather than isolated observations.

The work envisioned encompasses the design and analysis of algorithms, their coding (C++ and python), as well their experimental evaluation.

Conditions. Internship with *gratification*. Possibility to follow-up with a PhD thesis.

References

[1] H. Kamisetty, E.P. Xing, and C.J. Langmead. Free energy estimates of all-atom protein structures using generalized belief propagation. *Journal of Computational Biology*, 15(7):755–766, 2008.

[2] Ashish Vaswani, Noam Shazeer, Niki Parmar, Jakob Uszkoreit, Llion Jones, Aidan N Gomez, Łukasz Kaiser, and Illia Polosukhin. Attention is all you need. *Advances in neural information processing systems*, 30, 2017.

[3] Zilong Huang, Xinggang Wang, Lichao Huang, Chang Huang, Yunchao Wei, and Wenyu Liu. Ccnet: Criss-cross attention for semantic segmentation. In *Proceedings of the IEEE/CVF international conference on computer vision*, pages 603–612, 2019.

[4] Jonathan S Yedidia, William T Freeman, Yair Weiss, et al. Understanding belief propagation and its generalizations. *Exploring artificial intelligence in the new millennium*, 8(236-239):0018–9448, 2003.

[5] Jonathan S Yedidia, William T Freeman, and Yair Weiss. Constructing free-energy approximations and generalized belief propagation algorithms. *Information Theory, IEEE Transactions on*, 51(7):2282–2312, 2005.

[6] J. Jumper, R. Evans, A. Pritzel, T. Green, M. Figurnov, O. Ronneberger, K. Tunyasuvunakool, R. Bates, A. Žídek, A. Potapenko, et al. Highly accurate protein structure prediction with AlphaFold. *Nature*, 596(7873):583–589, 2021.