Chapter 8 Derivation of Quantum Associative Network from Hopfield-Like ANN and HNeT

8.1 CONNECTIONIST SIMULATIONS APPLIED FOR QUANTUM DYNAMICS

In Chapter 7, I have presented in detail how and where the mathematical formalism of associative ANN models by Hopfield and Haken is analogous to the mathematical formalism of quantum theory. In this Auxil. Chapter, I derive from associative ANN in a straight-forward way an original and fundamental quantum information processing model, or "algorithm", called the *Quantum Associative Network*. The initial ANN "algorithm" is presented first (sec. 8.2). It was chosen, because it is simple but nevertheless effective, technically realizable, and roughly (on global scale) biologically plausible, as a convenient one for presenting ANN-like and HNeT-like quantum information dynamics at a *fundamental* level.

DOI: 10.4018/978-1-61520-785-5.ch008

Copyright © 2011, IGI Global. Copying or distributing in print or electronic forms without written permission of IGI Global is prohibited.

200 Derivation of Quantum Associative Network from Hopfield-Like ANN and HNeT

The statement on rough biological plausibility needs justification. The "algorithm" is relatively biologically plausible on the level of uniform, bi-directionally denselyinterconnected network of some physiological units or formal neurons. As discussed in sec. 6.5, the neo-cortex globally meets such a description. Formal "neurons" could even be whole cortical (mini)columns. Additionally to such a macroscopic level, the "algorithm" is even much more implementable on the microscopic level of synapto-dendritic nets.

The Hopfield ANN model is mathematically equivalent to the theory of spinglass systems (i.e., amorphous assemblies of spins or small "magnets") (Mezard, Parisi & Virasoro, 1987; AuxLit 14). Spins are fundamental in (quantum) physics. Magnetic dipoles are considered as "macroscopic" spins. Electric dipoles, which are used in the holonomic theory (Pribram, 1991, Appendices with Jibu & Yasue), exhibit very similar collective dynamics. So, the present starting "algorithm" is potentially plausible for modelling the mentioned levels of the multi-level image processing in V1, but it must be properly constrained as discussed in section 4.6.

By extensive simulations of the quantum-implementable Hopfield-like ANN model and its generalizations using various concrete data sets, we have effectively realized parallel-distributed content-addressable memory, selective associative reconstruction of image-like patterns memorized in a compressed form.¹ We have found that the results depend very much on the correlation structure of a specific set of input patterns. In other words, beside the "hardware" (implementation) and the "software" ("algorithm"), also the "virtual software" (i.e., the input-data correlation structure) is essential. In sec. 8.5, results of my computational "recognition" of protein-patterns are briefly presented to show very successful performance of this "algorithm".

In the next section, I will present conventional associative ANN in a form which will be in sec. 8.4 translated to quantum formalism in a straight-forward way. I will start from a Hopfield-like ANN model in the approximation of linear activation function (central, "non-saturated" section of the tangens-hyperbolicus-like sigmoid function), because this is sufficient for associative processing and memory-storage, and suitable for our aim to implement information dynamics in a natural quantum system. Image processing is the most successful special case of the "algorithm's" application.

8.2 ASSOCIATIVE NEURAL NETWORKS

From now on, the terms like neural, neuron, synaptic connections, memory, association, learning, recognition, etc., will always be used in the formal sense of the present artificial neural net (ANN) theory. 16 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage: <u>www.igi-</u> <u>global.com/chapter/derivation-quantum-associative-network-hopfield/50507</u>

Related Content

Bring Out Your Data: The Evolution of the National Anesthesia Clinical Outcomes Registry (NACOR)

Thomas E. Grissom, Andrew DuKatz, Hubert A. Kordylewskiand Richard P. Dutton (2013). *Methods, Models, and Computation for Medical Informatics (pp. 126-145).* www.irma-international.org/chapter/bring-out-your-data/73075

Discovering Protein-Protein Interaction Sites from Sequence and Structure

David Laand Daisuke Kihara (2009). *Biological Data Mining in Protein Interaction Networks (pp. 64-79).*

www.irma-international.org/chapter/discovering-protein-protein-interaction-sites/5559

Transcriptomics to Metabolomics: A Network Perspective for Big Data

Ankush Bansaland Pulkit Anupam Srivastava (2018). *Applying Big Data Analytics in Bioinformatics and Medicine (pp. 188-206).* www.irma-international.org/chapter/transcriptomics-to-metabolomics/182947

Unsupervised Data Analysis Methods used in Qualitative and Quantitative Metabolomics and Metabonomics

Miroslava Cuperlovic-Culf (2012). Systemic Approaches in Bioinformatics and Computational Systems Biology: Recent Advances (pp. 1-28). www.irma-international.org/chapter/unsupervised-data-analysis-methods-used/60826

Interaction of Nucleic Acids: Hidden Order of Interaction

Gennadiy Vladimirovich Zhizhin (2021). *International Journal of Applied Research in Bioinformatics (pp. 1-8).* www.irma-international.org/article/interaction-of-nucleic-acids/278747