

INTRODUCTION

CNN is an acronym for either Cellular Neural Network when used in the context of brain science, or Cellular Nonlinear Network when used in the context of *coupled dynamical systems*. A CNN is defined by *two* mathematical constructs:

1. A spatially discrete collection of continuous nonlinear dynamical systems called *cells*, where *information* can be encrypted into each cell via three independent variables called *input*, *threshold*, and *initial state*.
2. A *coupling law* relating one or more relevant variables of each cell C_{ij} to all neighbor cells C_{kl} located within a prescribed sphere of influence $S_{ij}(r)$ of radius r , centered at C_{ij} .

In the special case where the CNN consists of a homogeneous array, and where its cells have no inputs, no thresholds, and no outputs, and where the sphere of influence extends only to the *nearest* neighbors (i.e. $r = 1$), the CNN reduces to the familiar concept of a *nonlinear lattice*.

Part I of this three-part exposition (reprinted from a theme issue on “Visions of Nonlinear Science in the 21st Century” of the *International Journal of Bifurcation and Chaos*, volume 7, numbers 9 & 10, 1997) is devoted to the *standard CNN equation*

$$\begin{aligned} \dot{x}_{ij} &= -x_{ij} + \sum_{kl \in S_{ij}(r)} a_{kl} y_{kl} + \sum_{kl \in S_{ij}(r)} b_{kl} u_{kl} + z_{ij} \\ y_{ij} &= f(x_{ij}) = \frac{1}{2} (|x_{ij} + 1| - |x_{ij} - 1|) \\ i &= 1, 2, \dots, M, j = 1, 2, \dots, N \end{aligned}$$

where x_{ij} , y_{ij} , u_{ij} and z_{ij} are *scalars* called *state*, *output*, *input*, and *threshold* of cell C_{ij} ; a_{kl} and b_{kl} are scalars called *synaptic weights*, and $S_{ij}(r)$ is the sphere of influence of radius r . In the special case where $r = 1$, a standard CNN is uniquely defined by a string of “19” real numbers (a uniform *threshold* $z_{kl} = z$, nine feedback synaptic weights a_{kl} , and nine control synaptic weights b_{kl}) called a *CNN gene* because it completely determines the properties of the CNN. The universe of all CNN genes is called the *CNN genome*. Many applications from image processing, pattern recognition, and brain science

can be easily implemented by a CNN “program” defined by a string of CNN genes called a *CNN chromosome*.

The first new result presented in this exposition asserts that *every* Boolean function of the neighboring-cell inputs can be explicitly synthesized by a CNN chromosome. This general theorem implies that *every cellular automata* (with binary states) is a CNN chromosome.

In particular, a constructive proof is given which shows that the *game-of-life* cellular automata can be realized by a CNN chromosome made of only three CNN genes. Consequently, this “game-of-life” CNN chromosome is a *universal Turing machine*, and is capable of *self-replication* in the Von Neumann sense [Berlekamp *et al.*, 1982].

One of the new concepts presented in this exposition is that of a *generalized cellular automata* (GCA), which is outside the framework of classic cellular (Von Neumann) automata because it *cannot* be defined by *local rules*: It is simply defined by iterating a CNN gene, or chromosome, in a “CNN DO LOOP”. This new class of generalized cellular automata includes not only *global* Boolean maps, but also *continuum-state cellular automata* where the *initial state configuration* and its *iterates* are *real* numbers, not just a finite number of states as in classical (von Neumann) cellular automata.

Another new result reported in this exposition is the successful implementation of an analog input analog output CNN universal machine, called a *CNN universal chip*, on a single silicon chip. This chip is a complete dynamic array stored-program computer where a CNN chromosome (i.e. a CNN algorithm or flow chart) can be programmed and executed on the chip at an extremely high speed of 1 Tera (10^{12}) analog instructions per second (based on a 100×100 chip). The CNN universal chip is based *entirely* on *nonlinear dynamics* and therefore differs from a digital computer in its fundamental operating principles.

Part II of this exposition is devoted to the important subclass of *autonomous CNNs* where the cells have *no inputs*. This class of CNNs can exhibit a great variety of complex phenomena, including pattern formation, Turing patterns, knots, autowaves, spiral waves, scroll waves, and spatiotemporal chaos. It provides a *unified paradigm for complexity*, as well as an *alternative paradigm* for simulating nonlinear partial differential equations (PDE’s). In this context, rather than regarding the autonomous CNN as an approximation of nonlinear PDE’s, we advocate the more provocative point of view that nonlinear PDE’s are merely idealizations of CNNs, because while nonlinear PDE’s can be regarded as a limiting form of autonomous CNNs, only a small class of CNNs has a limiting PDE representation.

Part III of this exposition is rather short but no less significant. It contains in fact the potentially most important *original* results of this exposition. In particular, it asserts that all of the phenomena described in the

complexity literature under various names and headings (e.g. *synergetics*, *dissipative structures*, *self-organization*, *cooperative and competitive phenomena*, *far-from-thermodynamic equilibrium phenomena*, *edge of chaos*, etc.) are merely *qualitative* manifestations of a more fundamental and *quantitative* principle called the *local activity dogma*. It is *quantitative* in the sense that it not only has a precise definition but can also be explicitly tested by computing whether a certain explicitly defined expression derived from the CNN paradigm can assume a negative value or not. Stated in words, the *local activity dogma* asserts that in order for a non-conservative system or model to exhibit any form of *complexity*, such as those cited above, the associated CNN *parameters* must be chosen so that either the *cells* or their *couplings* are *locally active*.