

## RECURSIVE GENOME FUNCTION OF THE CEREBELLUM: GEOMETRIC UNIFICATION OF NEUROSCIENCE AND GENOMICS

Andras J. Pellionisz<sup>1</sup>, Roy Graham<sup>2</sup>, Peter A. Pellionisz<sup>3</sup>, Jean-Claude Perez<sup>4</sup>

### Affiliation

<sup>1</sup> HolGenTech, President, Sunnyvale, California, USA, 94086, holgentech\_at\_gmail\_dot\_com

<sup>2</sup> DRC Computer, Vice President, Sunnyvale, California, USA, 94089

<sup>3</sup> UCLA Westwood, California, USA, 90024

<sup>4</sup> IBM Emeritus, Independent researcher, Martignas, France 33127

### Abstract

Recursive Fractal Genome Function in the geometric mind frame of Tensor Network Theory (TNT) leads through FractoGene to a mathematical unification of physiological and pathological development of neural structure and function as governed by the genome. The cerebellum serves as the best platform for unification of neuroscience and genomics. The matrix of massively parallel neural nets of fractal Purkinje brain cells explains the sensorimotor, multidimensional non-Euclidean coordination by the cerebellum acting as a space-time metric tensor. In TNT, the recursion of covariant sensory vectors into contravariant motor executions converges into Eigenstates composing the cerebellar metric as a Moore-Penrose Pseudo-Inverse.

The Principle of Recursion is generalized to genomic systems with the realization that the assembly of proteins from nucleic acids as governed by regulation of coding RNA (cRNA) is a contravariant multi-component functor, where in turn the quantum states of resulting protein structures both in intergenic and intronic sequences are measured in a covariant manner by non-coding RNA (ncRNA) arising as a result of proteins binding with ncDNA modulated by transcription factors. Thus, cRNA and ncRNA vectors by their interference constitute a genomic metric. Recursion through massively parallel neural network and genomic systems raises the question if it obeys the Weyl law of Fractal Quantum Eigenstates, or when derailed, pathologically results in aberrant methylation or chromatin modulation; the root cause of cancerous growth. The growth of fractal Purkinje neurons of the cerebellum is governed by the aperiodical discrete quantum system of sequences of DNA bases, codons and motifs. The full genome is fractal; the discrete quantum system of pyknon-like elements follows the Zipf-Mandelbrot Parabolic Fractal Distribution curve.

The Fractal Approach to Recursive Iteration has been used to identify fractal defects causing a cerebellar disease, the Friedreich Spinocerebellar Ataxia – in this case as runs disrupting a fractal regulatory sequence. Massive deployment starts by an open domain collaborative definition of a standard for fractal genome dimension in the embedding spaces of the genome-epigenome-methylome to optimally diagnose cancerous hologenome in the nucleotide, codon or motif-hyperspaces. Recursion is parallelized both by open domain algorithms, and also by proprietary FractoGene algorithms on high performance computing platforms, for genome analytics on accelerated private hybrid clouds with PDA personal interfaces, becoming the mainstay of clinical genomic measures prior and post cancer intervention in hospitals and serve consumers at large as Personal Genome Assistants.

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