COMPUTER SIMULATION OF THE CEREBELLAR NEURONAL NETWORK

(Cinematized Cerebellar Activity Model)

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The structure of the cerebellar neuronal network, which is better known than any other part of the nervous system, offers challenging theoretical problems regarding structure-function relationships, which are too complex to be resolved without the help of computer simulation. Earlier attempts have been made, therefore, to simulate the cerebellar activity by digital computers. Pellionisz, 1970, 1972a. However, not knowing the exact numerical relations of various neuron types and with only marginal understanding of the main geometric parameters of the network, excessive simplifications have been made in the model, which have been found later to be unjustified. A recent systematic quantitative histological study of the cerebellar cortex /Palkovits et al., 1971a, b, c, 1972/ enabled the authors to develop a new, more realistic connectivity model, for a discrete single unit network simulation to be based on. This simulation model, presented in the Congress, is elaborated in detail in Pellionisz and Szentagothai, 1972.

The program performed on a CDC 3300 computer simulates the spatio-temporal activity of about 30000 neurons in a 100 ms period of time. The hypothesis that Golgi cell inhibition is to keep the density of excited parallel fibers in a narrow range both within time and space, has been tested by the model with special attention of the possible role of the 2-3 fold inputs to the Golgi cells. The results of the simulation support this hypothesis and indicate that: 1. the Golgi cells are activated basically directly by mossy afferents; 2. the indirect parallel fiber input improves the efficiency of the Golgi cell inhibition by speeding up its development and by increasing its long-term stability; 3. the Golgi cell inhibition would be an extremely inefficient mechanism if this would act as coinciden-

References

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