

## DYNAMIC SINGLE UNIT SIMULATION OF A REALISTIC CEREBELLAR NETWORK MODEL

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### SUMMARY

On the basis of recent quantitative histological analysis of the cerebellum a single unit simulation model of the neuronal network was developed to study some spatio-temporal aspects of its activity. The hypothesis that Golgi inhibition serves to keep the density of excited parallel fibers in a narrow range both in time and in space has been tested, with special attention to the possible role of the 2-fold input to the Golgi cells. The result of the simulation supports the hypothesis in showing that: (i) marked 'leveling' of activity occurs, basically as a result of mossy fiber-driven Golgi cell action, (ii) the indirect (parallel fiber) input appears to improve the efficiency of the mechanism by increasing the speed of development and stabilizing the long-term accuracy of the leveling, and (iii) a precondition of such an effect is, however, that Golgi cells do not act as coincidence detectors, but can be fired independently either by direct or indirect inputs.

By modeling the spatio-temporal single unit activities of about 30,000 cells in the time interval of 0-100 msec after random excitation it was possible to cinematize the changing activity patterns of the various neuronal elements for visual inspection, and to process the data obtained from various points of view. This mode of approach might aid the confrontation and comparison of histological and electrophysiological results, and their synthesis into new concepts of the activities of neuronal networks.

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### INTRODUCTION

The neuronal network of the cerebellar cortex offers challenging theoretical problems regarding structuro-functional relationships, which are too complex to be resolved without the help of computer simulation. Fortunately, the network has unique structural properties that favor such modeling. It (1) is built up of only 5 different types of neuron; (2) has two characteristically different input channels; and