on the electrochemical properties of the devices. The neural probes were fabricated with 8 or 6 microelectrodes, through standards microfabrication techniques. Planar microelectrodes (28 mm in diameter) were fabricated on the SU-8 based neural probe. The gold electrodeposition on titanium microelectrode was carried using a standard three-electrodes configuration in solution for concentrations of 4.5, 9 or 18 mM of at cathodics current of 25 nA, 125 nA, 250 nA and 1000 nA (pH 8). Electrochemical characterization was realized by cyclic voltammetry and impedance spectroscopy using ferricyanite and phosphate-buffered saline. **Results:** We identified quasi-reversible faradic processes close to the microelectrode surface and an interval in which the microdevice could be used in electrophysiological recording (or stimulation). The mean microelectrode's impedance was found to be 26.6 ± 5.5 kΩ at 1kHz. Furthermore, the effective areas of the microelectrodes were calculate and analyzed by optical microscopy images to verify the geometry of the microelectrodes. Finally, the device was applied in glutamate solution to evaluate its application as potential electrochemical sensor. Discussion: It was found that increasing the scan rate adds the amount of electroactive species to the metal. Furthermore, It was found that both the concentration of and the current are important parameters in controlling the morphology of the electrodeposited gold. **Conclusion:** In order to understand the possibility of mechanisms of tissue trauma, we identified quasi-reversible faradic processes close to the microelectrode surface and an interval in which the microdevice could be used in electrophysiological recording (or stimulation).

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On-line Gated Learning Action Selection in a Biologically Inspired Cognitive Architecture

K. Raizer[1], A.L.O. Paraense[2], S. Mapa[2] , R.R. Gudwin[2]

[1]Artificial Cognition Group, FEEC, University of Campinas-UNICAMP, São Paulo, Brazil.

Introduction: In this work we extend GLAS,[1] a Gated Learning Action Selection algorithm inspired by the computational neuroscience model described in the Leabra framework.[2] Adapting Leabra's PBWM (Prefrontal Cortex Basal Ganglia Working Memory) mechanism to provide human-readable solutions was motivated by our will to provide a robotic wheelchair assistive agent[3] with the capacity to learn the patient's preferences. However, in order for it to learn by on-line interacting with the environment, we have embedded it into a biologically inspired cognitive architecture.[4] **Materials and Methods:** For this experiment we used the cognitive architecture described in,[4] and the learning algorithm described in.[1] Five codelets (small pieces of code, each specialized in a specific task) were developed for dealing with each aspect of the cognitive process, as seen in Figure 1. The agent starts with a random stimuli/action-selection policy, and must learn the rules for the 1-2 AX Working memory Task.[2] **Results:** Figure 2 shows that the algorithm converges to a solution tree with 7 nodes around iteration 5. At this point, it is able to solve the 1-2 AX task. **Discussion:** The cognitive architecture is now able to learn by interacting with the simulated environment. We now intend to validate it with the robotic wheelchair assistive agent by making it learn the patient's preferences, so it can give him relevant suggestions. Conclusion: This paper has presented a method for embedding GLAS into a biologically inspired cognitive architecture and giving it the capacity to learn by on-line interaction. **Supported by:** CAPES, FAPESP and the CNPq for the financial support.

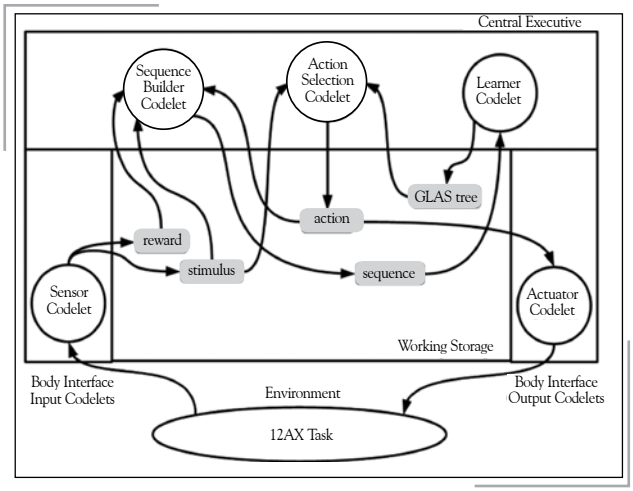

Figure 1

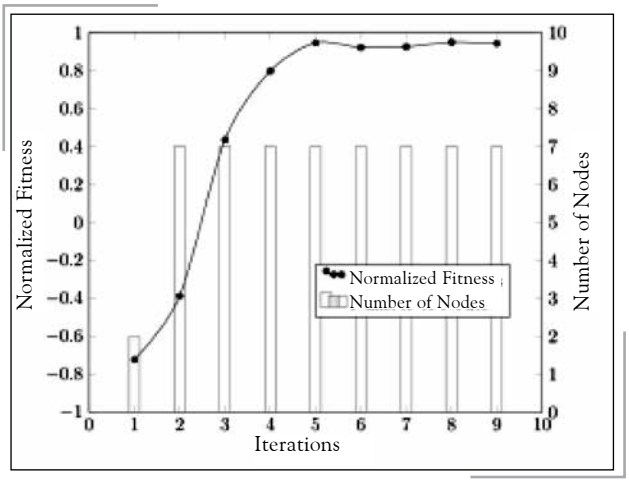

Figure 2

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Improving the Efficiency of Whole Exome Variant Analysis Through the Parallelization of Its Computer Process

L.L. Cendes[1], W. Souza[1], B. Carvalho[1], I. Lopes-Cendes[1]

[1]Laboratory of Biostatistics and Computational Biology, Department of Medical Genetics, School of Medical Sciences, University of Campinas-UNICAMP, São Paulo, Brazil and Brazilian Institute of Neuroscience and Neurotechnology (BRAINN)

Introduction: The Genome Analysis Toolkit, also known as GATK, is a set of tools designed to analyze molecular data obtained through Next-Generation Sequencing (NGS) and identify variants that may be associated to phenotypes like disease status and drug response.[1] It consists of several walkers, each one serving a different function. The Realigner Target Creator identifies genomic intervals that may contain either sequencing or alignment errors. These intervals will be used by the next module, the Indel Realigner, which locally realigns the reads to correct misalignments that happen due to the presence of insertions and deletions. The Base Recalibrator then takes the output of the Indel Realigner and subjects it to the first pass of the base quality score recalibration. The Print Reads module renders the output of the Base Recalibrator to a binary file format, referred to as BAM file. The Haplotype Caller takes the output of the Print Reads and calls insertions, deletions and SNPs through the re-assembly of haplotypes in an active region.[2] There is a framework of the GATK software, called Queue, which uses a QScript to run multi-stage genomic analysis.[3] It supports three different types of parallelization: A) data threads; B) CPU threads; and C) scatter-gather strategy. The latter manages the number of pieces in which the input files will be divided, processed and later gathered into a final summary. The scatter-gather method can by parallelized by the GridEngine or its variants.[4] In this project, we implemented a QScript tool