

X-CORESIM - Public Abstract

What determines the human potential? Are we merely genetic machines programmed with evolutionary algorithms evolved through the struggle of eons? Are all our efforts, personal battles, education and training merely futile attempts to improve a model that was locked into place by nature? Although those questions have been posed by mankind since time immemorial, today's technological progress promises to unlock these secrets for the very first time in history. It is commonly known that our brain is made up of neurons and synapses; their interaction produces not only thoughts and reactions, but also forms what we call personality, habits, and more – the entirety of this 'wiring' of the brain is called the 'connectome'.

A thorough understanding of the connectome would open up numerous possibilities – we could grasp the determining factors of personality, develop new methods to heal the brain effectively after disruptive diseases and injuries, cure depression and anxiety without the use of drugs, maybe even extend the human potential altogether. In psychology and healthcare we could derive better models of mental disorders, the effects of the environment on the brain (psychological or chemical), and simulate the impact of future drugs without cruel experiments. Beyond all possible applications regarding humans, comprehending the emergence of animal connectomes could reveal the basic workings of evolution itself.

However, as the human connectome consists of roughly 86 billion neurons (and an estimated 100-1,000 trillion synapses), which is thoroughly beyond our reach to simulate, it is necessary to start with a smaller organism whose brain structure has already been mapped. Therefore, we will focus our research on the workings of the *c.elegans* worm's connectome, which consists of only 302 neurons and several thousand synapses, allowing us to apply modern algorithms running on commodity hardware (even laptops and tablets). Moreover, it is our goal to offer a Web-based research platform enabling experts outside the fields of IT (especially biomed and medicine) to run experiments without any programming knowledge.

Our work will therefore consist of three stages: 1) First, we need to find a 'base model' (the parameters) of the *c.elegans*, for which we will design evolutionary algorithms and perform experiments on a dataset provided by the OpenWorm foundation. 2) Upon this we will implement a Web-based simulation of the connectome, comprising visualization and interaction with the structure. In order to facilitate further experiments by us as well as domain experts, we will conceive a domain specific language (DSL) for querying and manipulating connectomes. 3) Based on this previous work, we will investigate how much 'stress' a connectome can tolerate before stable behavioral patterns collapse (resilience). Our findings will be published in biomed as well as computer science journals and our software be open-sourced.