**X-CORESIM - Public Abstract**

The interactions of neurons and synapses in our brain are responsible for learning and intelligence and the entirety of this “wiring” of our brain is called the “connectome”. The enormous importance of understanding the human connectome is manifold, as a thorough understanding of the connectome would open up numerous possibilities – we could grasp the determining factors of personality, develop new methods for curing the brain effectively after disruptive diseases and injuries, find new treatments for depression and anxiety without the use of drugs, etc. In psychology and biomedicine, 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 painful experiments. Beyond all possible applications regarding humans, comprehending the emergence of animal connectomes could reveal the fundamentals of evolution itself.

However, 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. Consequently, 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 tablet computers). However, any research in this area needs much algorithmic understanding and programming expertise. Therefore one goal of our project is to provide a Web-based research platform enabling non-computing experts, e.g. biologists or biomedical scientists to carry out sophisticated 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 novel evolutionary algorithms and perform experiments on a data set provided by the OpenWorm foundation.

2) Upon this we will implement an open-source Web-based connectome simulation comprising visualization and interaction with the network. 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 and their constituting elements.

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 presented to the scientific community at international workshops and conferences and published in journals for the benefit of stimulating future work, which would not be possible without our fundamental research.