**A novel causal modeling algorithm uncovers predictive coding properties of c. elegans**

**Background**

Predictive coding is a theory in theoretical and cognitive neuroscience which aims to prove that the brain is

In other words, can the organism anticipate future environmental factors based on the information and inference it has accumulated in the past?

**Proposal**

In my proposal I identify a computational method not commonly used to investigate this specific theory of predictive coding. I further attempt to expand on this method by optimizing it

**Specific Aims**

**Aim 1 - Optimization of the Simplex Algorithm for Convergent Cross mapping (CCM)**

Convergent Cross Mapping Model is a type of tool for short range forecasting of chaotic time series data. The reason it is

However due to the nature of the algorithm, I believe there are certain repetitive motifs within the time series data that are not utilized by the algorithm, and may therefore lead to less than accurate inferences about the nature and strength of causal relationships among datasets. In addition, this may also lead to a weaker predictive ability. The

Aim 1.2

There are additional

**Aim 2 - Establishing causal relationships among neuronal subtypes within *c. elegans* time series dataset using modified Simplex Algorithm**

**Aim 3 – Using Modified Simplex on Additional Time Series Data**

I will use additional time series datasets to test the robustness of my

Allen Brain Atlas, OpenNeuro, CRCNS (Collaborative Research in Computational Neuroscience)

**Significance**

The advantages and impact of using this modified method in this unique way cannot be understated. Although predictive coding as a phenomenon has been characterized in more complex mammalian systems such as the human visual cortex, its presence has not been investigated to the same extent in less complex, non-mammalian, and non-spiking organisms. There is of publicly available time series data The use of nonlinear forecasting has predominantly been in ecological systems. Not only can this modified simplex method could be used on time series data in nonlinear complex systems, but it would be more suitable to the specific motifs that are found in c. elegans calcium traces, and other

**Figure 1**

**References**

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