

A classification model for rhythmic behavior in *Caenorhabditis elegans*

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Academic Disciplines:
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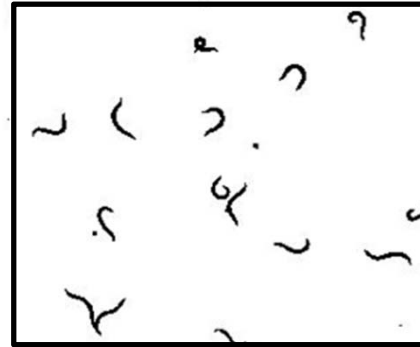
RESEARCH OBJECTIVE

C. elegans is a model organism used to study protein misfolding diseases such as Alzheimer's and Huntington's disease. We use engineering principals to create an analysis tool that uses the worm bending frequency patterns to detect and classify the extent of disease in muscle or neuronal cells. Better diagnosis in worms could lead to better research into human health and disease prevention.

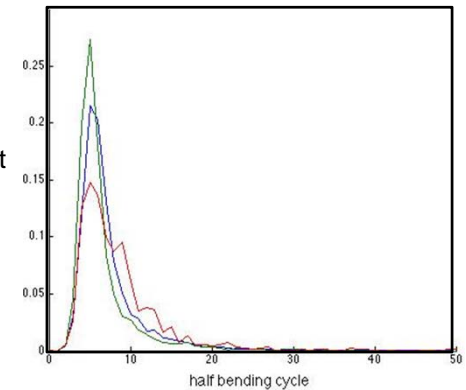
Worms strains with varying degrees of protein aggregation are tested.



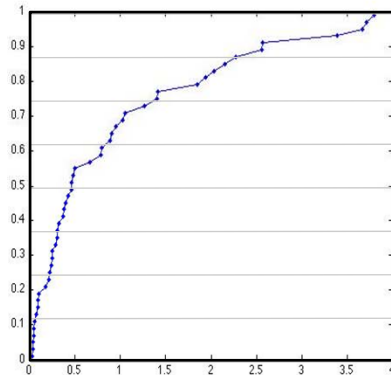
Videos of worms are analyzed to quantify the movements of worms and to calculate the half bending cycles.



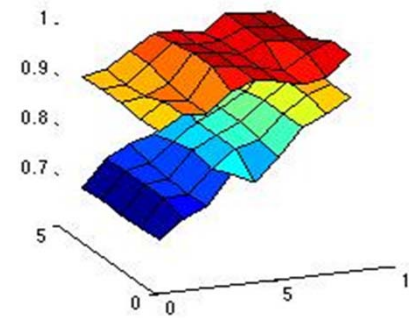
The half bending cycles from worms in different conditions have different distributions.



A finite measurement of the half bending cycle time distribution of individual worms is used as a feature space for classification model.

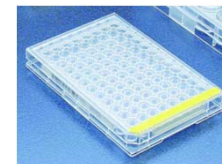


We tested the method of Support Vector Machine with Soft Margin and optimized the classification model over three data pre-processing parameters.



The worm population with less severe aggregation show a heterogeneity of bending behaviors and incorporating this would improve the performance of the classification model.

Fraction of Correct classification over data pre-processing parameters



The further development of this framework is to design a tool that will be applicable for high throughput drug and genetic screens.