

First Major Project

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Mus musculus



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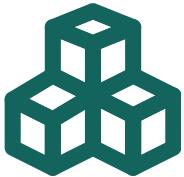


Problem Statement

The objective is to identify subsets of proteins that are discriminant between different classes of mice. The dataset includes protein expression levels in the cerebral cortex of both control and Down syndrome mice subjected to context fear conditioning. The aim is to classify the mice into eight distinct classes based on genotype, behavior, and treatment.



Objectives



Classify Mice Based on Protein Expression

Develop a machine learning model to accurately classify mice into one of the eight classes based on the expression levels of 77 proteins. These classes are determined by a combination of genotype (control or trisomic), behavior (stimulated to learn or not), and treatment (saline or memantine).



Identify Key Discriminant Proteins

Utilize feature selection techniques to identify which proteins or protein modifications are most important for distinguishing between the different classes. Understanding which proteins are key discriminators can provide insights into the biological mechanisms underlying learning and memory in Down syndrome.



Evaluate the Impact of Genotype, Behavior, and Treatment

Analyze the effect of genotype (control vs. trisomic), behavior (context-shock vs. shock-context), and treatment (saline vs. memantine) on protein expression levels. This includes evaluating how these factors influence associative learning and the potential therapeutic effects of memantine in trisomic mice.

Dataset Information

- **Instances:** 1080 (15 measurements per protein per mouse)
- **Features:** 80 (77 proteins + 3 additional features: Mouse ID, Genotype, Treatment)
- **Classes:** 8 (combination of genotype, behavior, and treatment)

Classes Information

01

c-CS-s

control,
stimulated, saline

02

c-CS-m

control,
stimulated,
memantine

03

c-SC-s

control, not
stimulated, saline

04

c-SC-m

control, not
stimulated,
memantine

05

t-CS-s

trisomic,
stimulated, saline

06

t-CS-m

trisomic,
stimulated,
memantine

07

t-SC-s

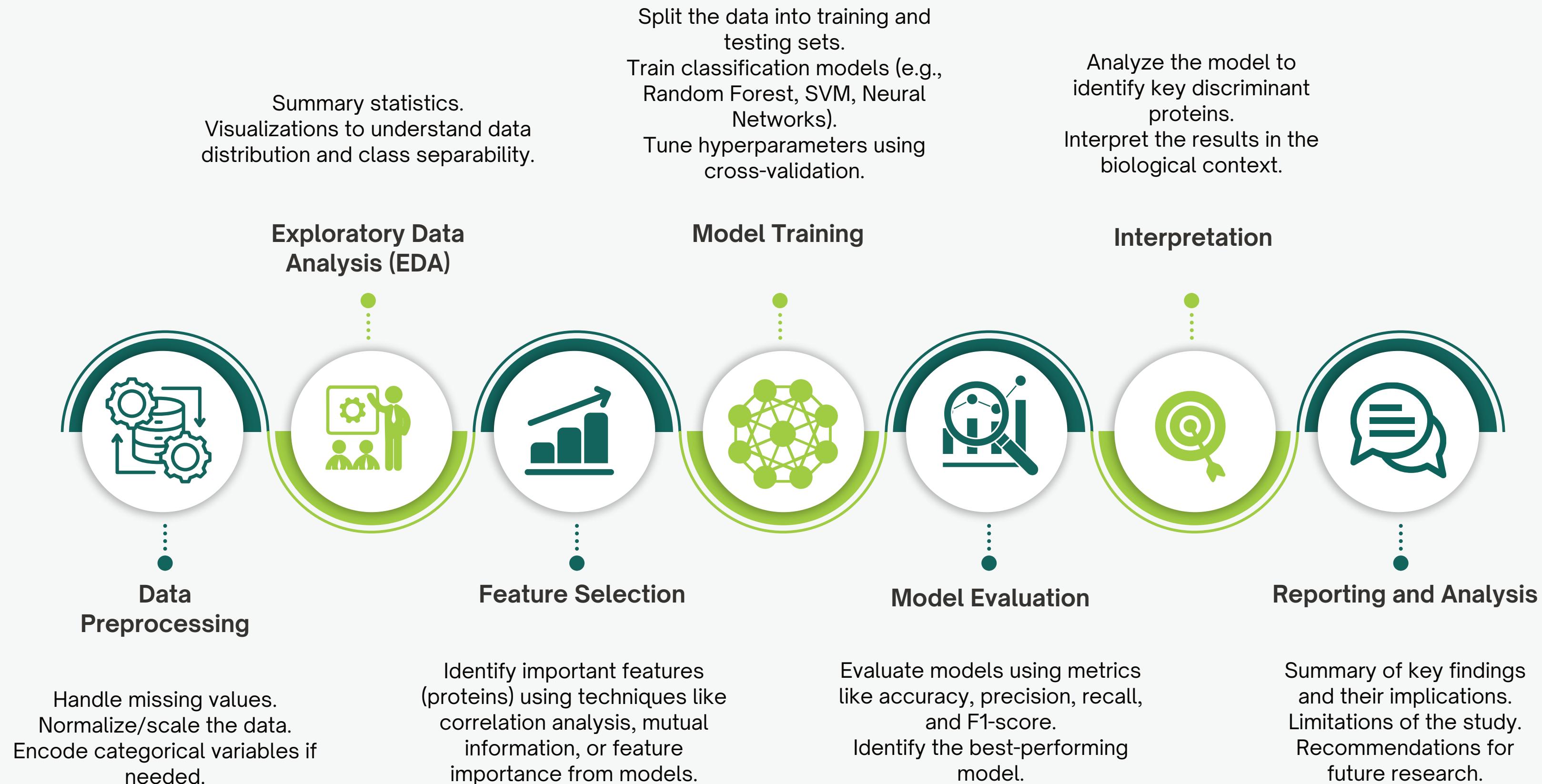
trisomic, not
stimulated, saline

08

t-SC-m

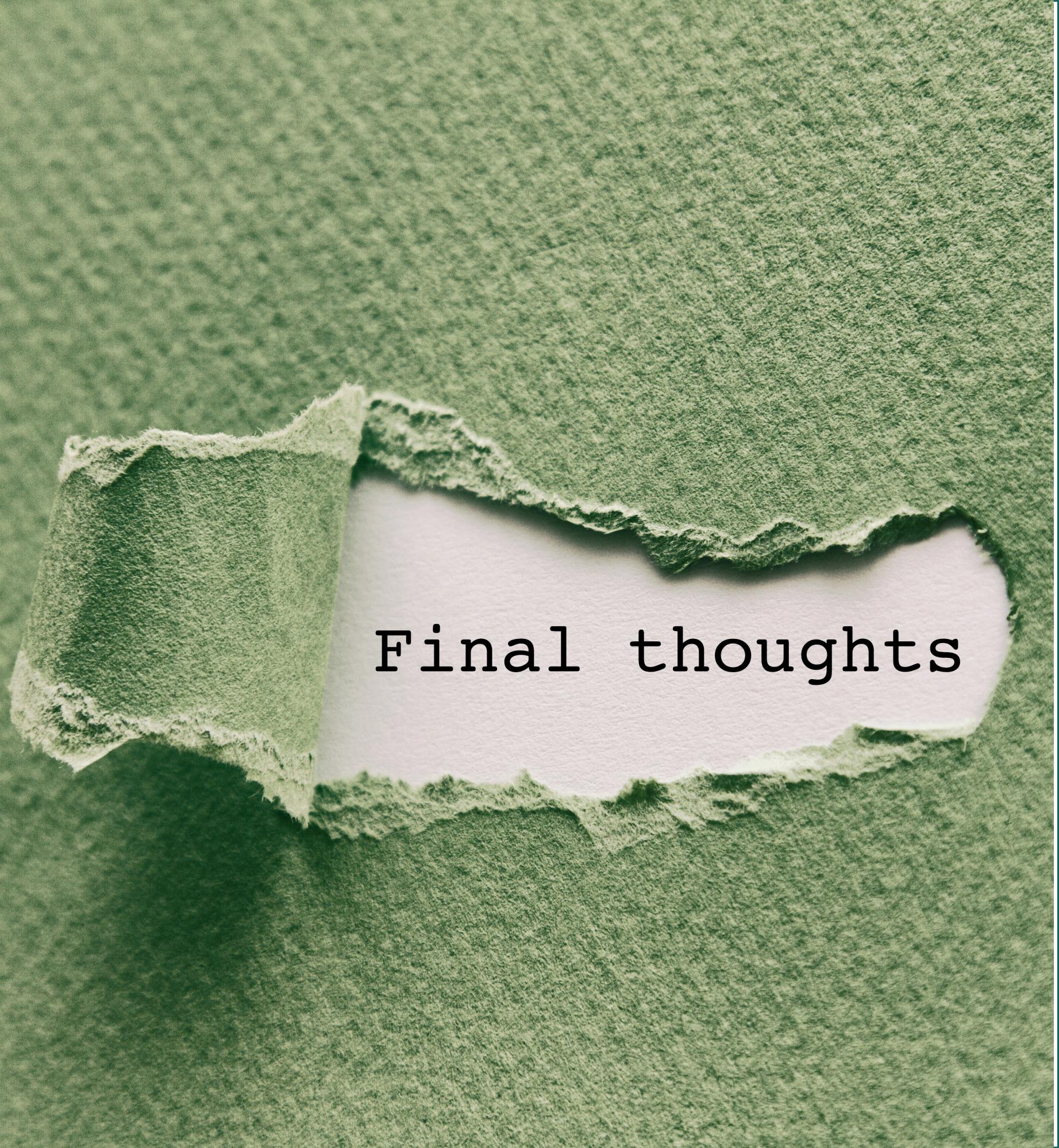
trisomic, not
stimulated,
memantine

Steps Involved



To Summarize

This project aims to utilize machine learning techniques to classify mice based on protein expression data and to uncover the biological significance of the identified proteins. By following the outlined steps, we can develop a robust model for classification and gain insights into the effects of genotype, behavior, and treatment on protein expression.



Final thoughts



THANK YOU

We wish you good luck.

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