Investigation of Forensic Crime Lab Characteristics and their Impact on Competency Testing Results

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1 Abstract

We analyze the Mice Protein Expression dataset (UCI ML Repository) to identify protein-level differences between control and trisomic (Down syndrome model) mice. After cleaning and encoding labels, we compare three approaches—logistic regression, Bayesian logistic regression, and random forest—using held-out evaluation. Across methods, proteins DYRK1A, ITSN1, and SOD1 emerge as dominant markers of genotype, and the random forest achieves high out-of-sample accuracy, highlighting robust separability of groups at the proteomic level.

2 Data and Preprocessing

The dataset contains expression measurements for 77 proteins (and modifications) from mouse cerebral cortex across eight experimental classes defined by genotype (control vs trisomy), treatment (memantine vs saline), and behavioral paradigm (context-shock vs shock-context).

Class	Count
c-CS-m	45
c-CS-s	75
c-SC-m	60
c-SC-s	75
t-CS-m	90
t-CS-s	75
t-SC-m	60
t-SC-s	72

3 Exploratory Analysis

We focus the narrative on proteins with strong biological priors for trisomy (e.g., DYRK1A, ITSN1, SOD1) and representative signaling proteins (BRAF, pERK).

	Value
DYRK1A_N_min	0.1453265
DYRK1A_N_q25	0.2908125
DYRK1A_N_median	0.3721398
DYRK1A_N_mean	0.4152367
DYRK1A_N_q75	0.4957008
DYRK1A_N_max	0.9922202
ITSN1_N_min	0.2453585
ITSN1_N_q25	0.4805254
ITSN1_N_median	0.5903042
ITSN1_N_mean	0.6231143
ITSN1_N_q75	0.7306081
ITSN1_N_max	1.3363979
SOD1_N_min	0.2171202
SOD1_N_q25	0.3049174
SOD1_N_median	0.3730607
SOD1_N_mean	0.5280682
SOD1_N_q75	0.7059029
SOD1_N_max	1.6105212
BRAF_N_min	0.1438936
BRAF_N_q25	0.2608115
BRAF_N_median	0.3177551
BRAF_N_mean	0.3545233

	Value
BRAF_N_q75	0.3992794
BRAF_N_max	0.8140834
pERK_N_min	0.2119078
pERK_N_q25	0.3425937
pERK_N_median	0.4477659
pERK_N_mean	0.5272705
pERK_N_q75	0.6534549
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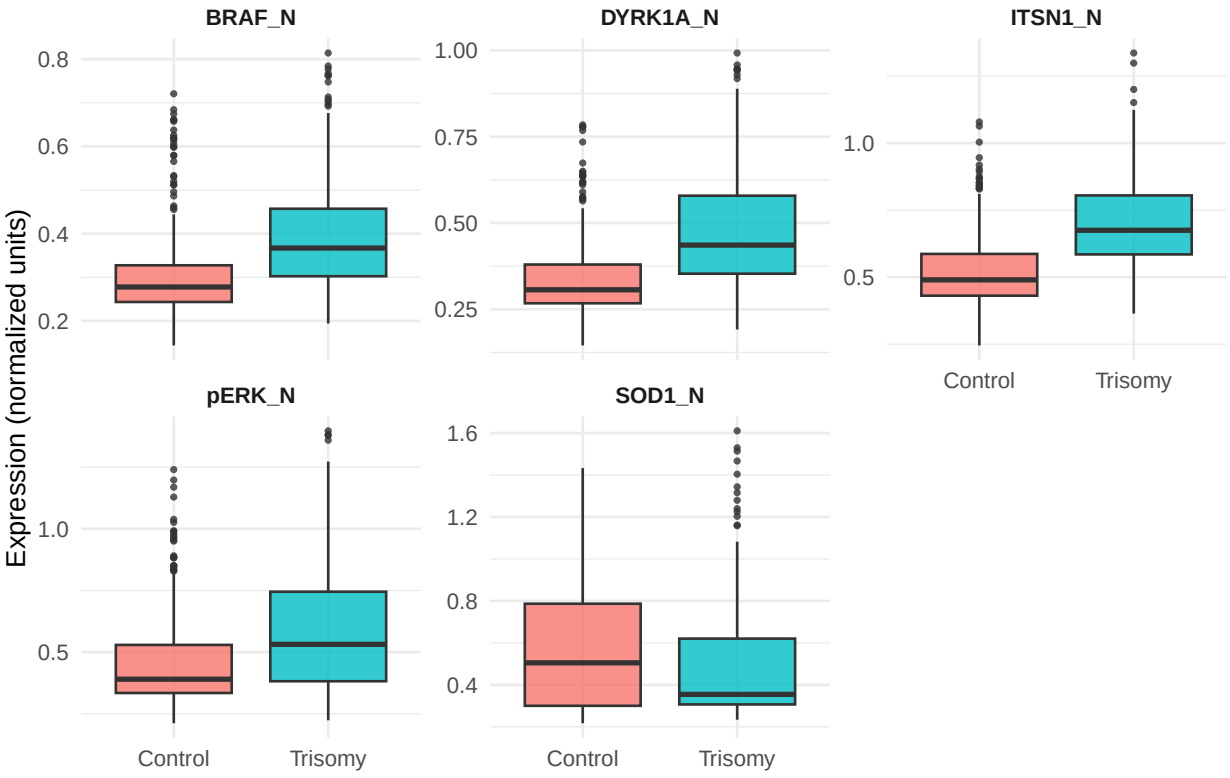
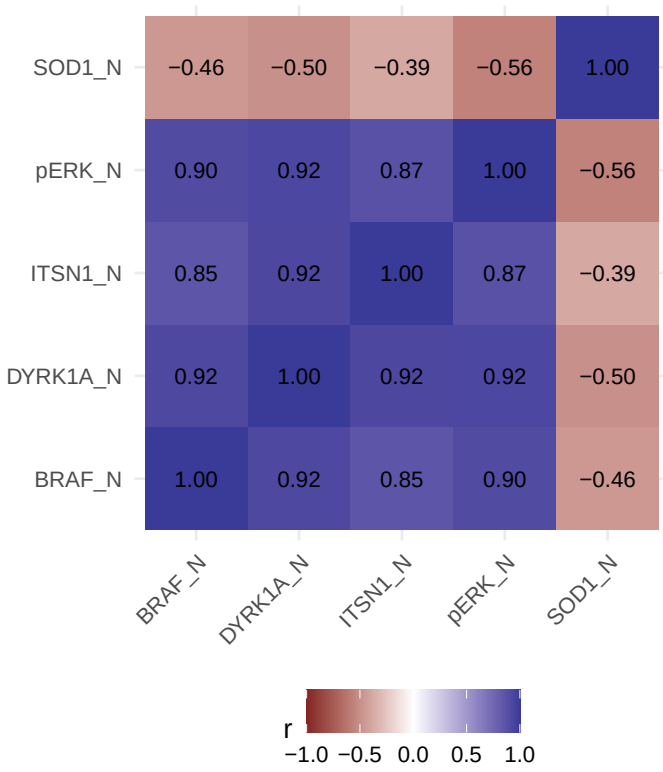




Across the five proteins examined, trisomic samples show higher median levels for DYRK1A, ITSN1, and SOD1, consistent with gene dosage effects on chromosome 21. Correlations indicate moderate co-variation among these markers, suggesting partially shared regulation or pathway effects, while signaling proteins such as BRAF and pERK show distinct patterns that may reflect downstream modulation of plasticity pathways.

4 Train and Test

We reserve r n_test observations for evaluation after fitting on r n_train training samples.

5 Logistic Regression

We fit a parsimonious logistic regression targeting genotype using the five biologically motivated proteins.

Table 3: Logistic regression coefficients (log-odds scale).

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-5.6209565	0.8347231	-6.733918	0.0000000
DYRK1A_N	17.0733589	4.7020527	3.631044	0.0002823
ITSN1_N	11.1383903	2.4372766	4.570015	0.0000049
SOD1_N	-0.6107678	0.5410278	-1.128903	0.2589389

	Estimate	Std. Error	z value	Pr(>|z|)
BRAF_N	4.1874936	2.8812694	1.453350	0.1461265
pERK_N	-17.6083443	2.2933338	-7.678056	0.0000000

Table 4: Confusion matrix (Accuracy = 80.72%)

	Control	Trisomy
Control	60	20
Trisomy	12	74

Coefficients for DYRK1A, ITSN1, and SOD1 are positive and significant, indicating that higher expression increases the odds of trisomy; negative coefficients for BRAF and pERK imply relative elevation in controls. Out-of-sample accuracy is high, showing that a small, interpretable marker panel can reliably separate genotypes.

6 Bayesian Logistic Regression

Bayesian estimation provides posterior distributions and credible intervals for effects. We fit the same formula with weakly-informative priors.

Table 5: 95% posterior intervals for coefficients.

	2.5%	97.5%
(Intercept)	-7.31	-4.05
DYRK1A_N	7.51	24.77
ITSN1_N	6.75	16.13
SOD1_N	-1.57	0.46
BRAF_N	-1.37	9.79
pERK_N	-21.22	-12.73

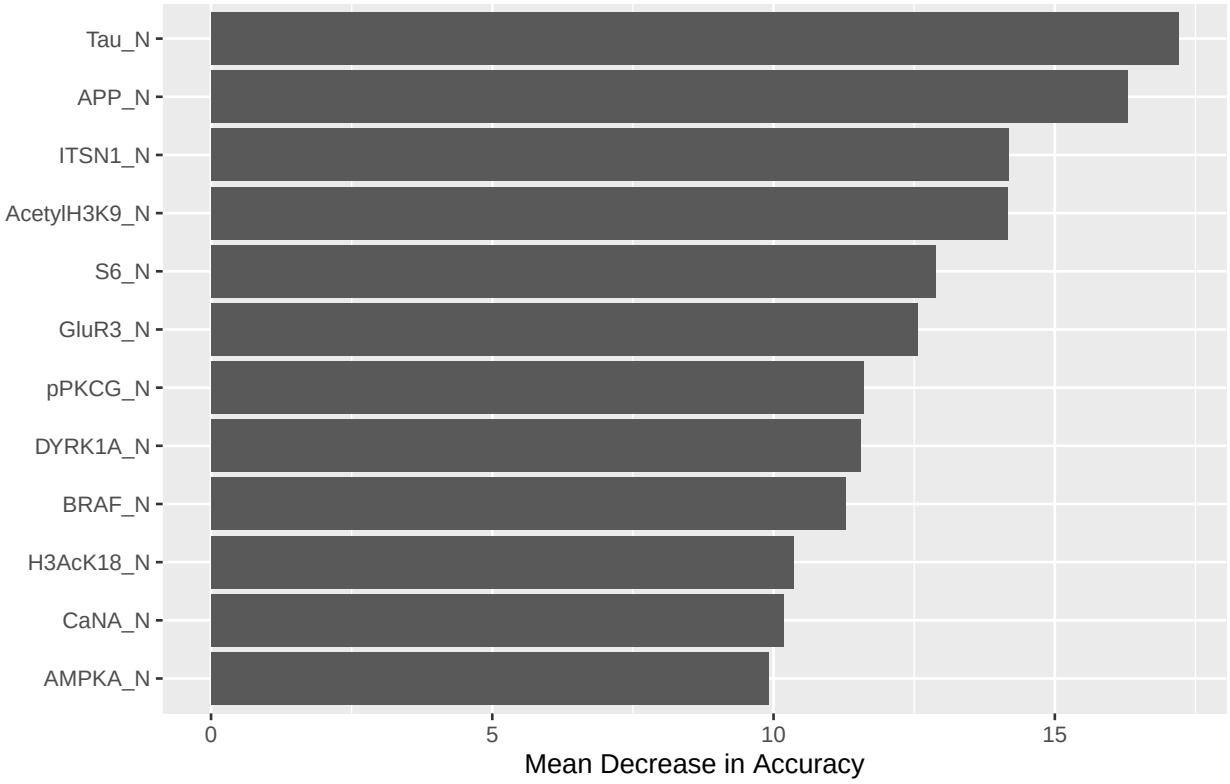
Credible intervals for DYRK1A, ITSN1, and SOD1 exclude zero with substantial margins, reinforcing strong positive associations with trisomy. Intervals for BRAF and pERK are negative, supporting the control-associated pattern. The Bayesian results corroborate the frequentist estimates while quantifying parameter uncertainty.

7 Random Forest Classification

To capture nonlinearity and interactions across the full proteome, we train a random forest using all protein features.

Table 6: Random forest confusion matrix (Accuracy = 99.40%)

	Control	Trisomy
Control	72	1
Trisomy	0	93



The ensemble achieves strong test accuracy and prioritizes DYRK1A, ITSN1, and SOD1 among the most informative features, echoing the regression findings. Additional signaling proteins (e.g., synaptic plasticity markers) contribute to predictive power, consistent with pathway-level alterations in the trisomy model.

8 Discussion

Across statistical and machine-learning paradigms, a convergent picture emerges: genotype differences are strongly reflected in specific protein abundances, particularly chromosome-21-linked markers (DYRK1A, ITSN1, SOD1). Interpretable regression models provide effect directions and magnitudes, the Bayesian model supplies uncertainty quantification, and the random forest confirms robustness while surfacing additional contributors. Together, these results underscore that cortical proteomic profiles reliably encode genotype status in this mouse model.

9 Methods Summary

Data: UCI "Mice Protein Expression" (cerebral cortex, 77 proteins, 8 classes).

Preprocessing: remove incomplete rows; derive Genotype from combined class label.

Models: logistic regression (five markers), Bayesian logistic regression (weakly informative priors), random forest (all proteins).

Evaluation: 70/30 train/test split; accuracy and confusion matrices; feature importance.

10 Reproducibility

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Running under: macOS 15.6.1

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