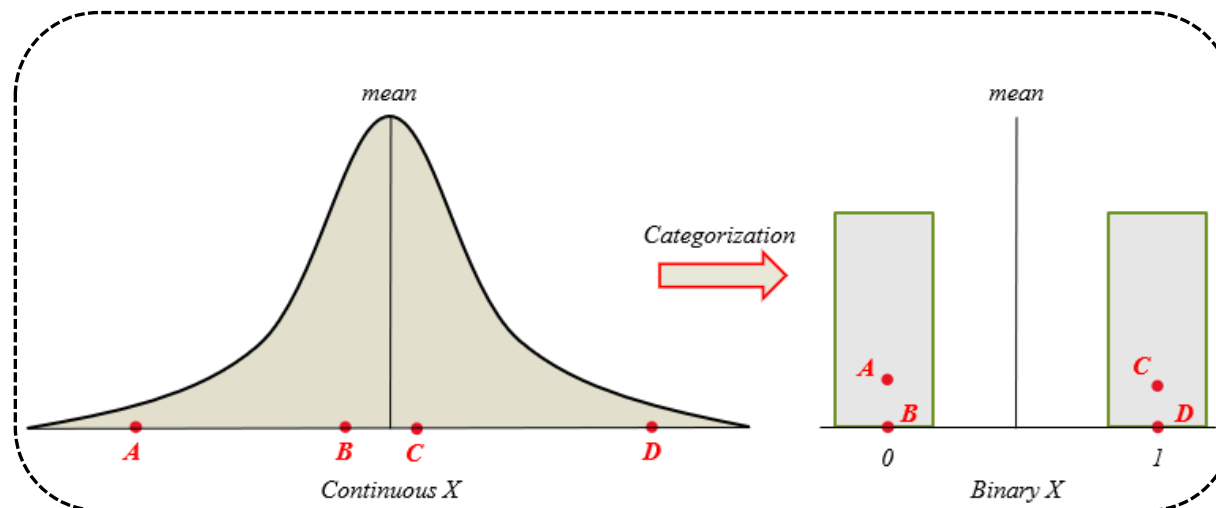


Categorizing Continuous Data in QSAR

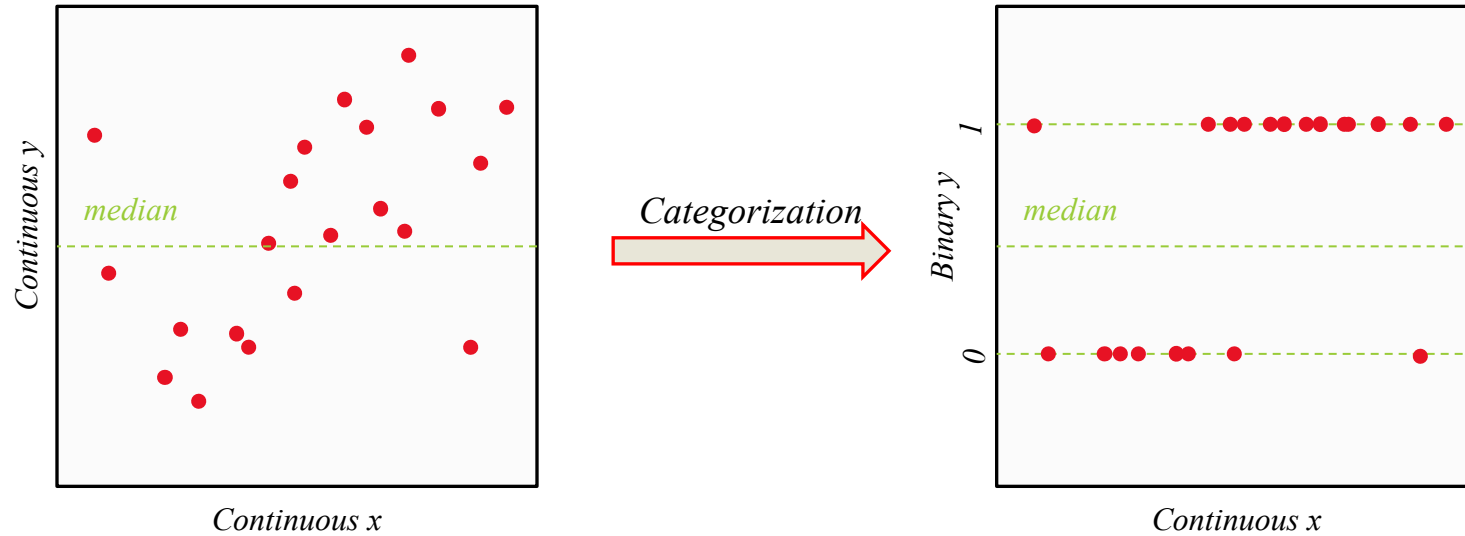


Scott Kolmar

*U.S. Environmental Protection Agency
Center for Computational Toxicology and Exposure
March 21st, 2022*

This presentation does not reflect EPA policy.

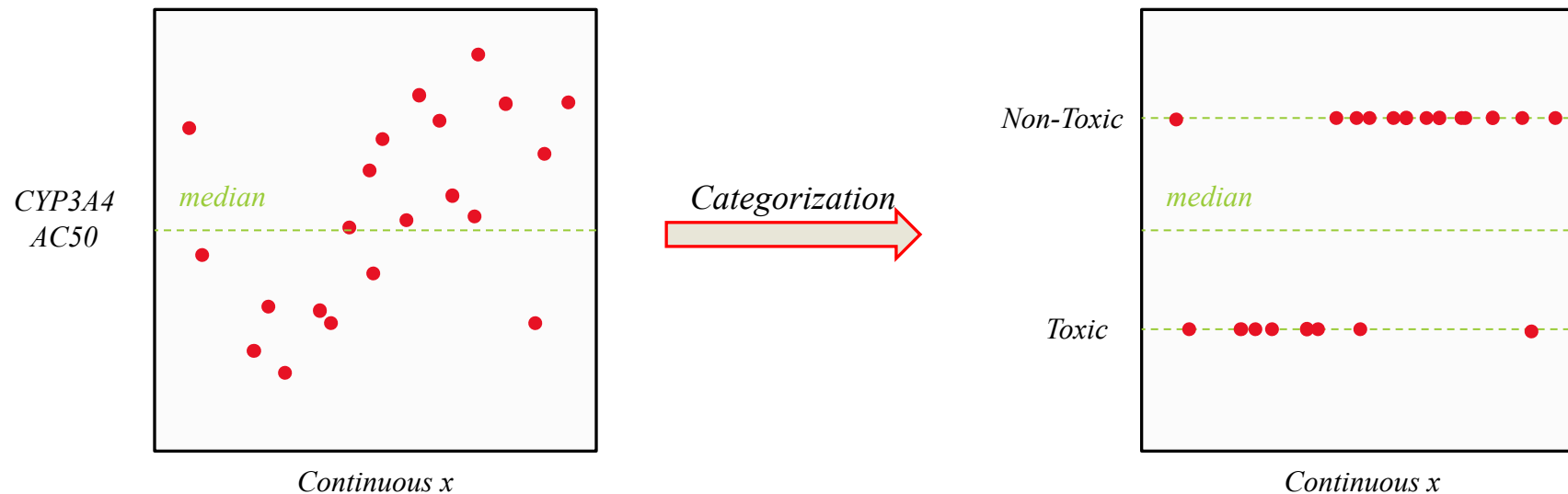
Splitting Data



Modelers often split (categorize) *continuous data* into *categorical data*

This leads to a *loss of information*, *loss of effect size*,
and *loss of statistical significance* between variables

Splitting Data

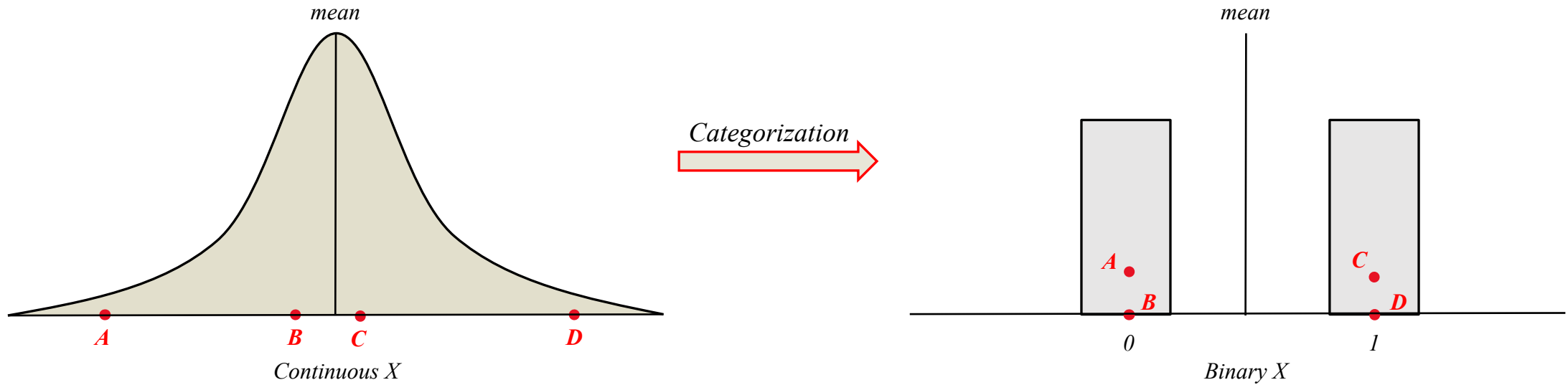


For ADME modeling:

Separate lead compounds into “Non-Toxic” and “Toxic” bins by splitting them on some enzyme activity threshold

- It is far more informative to predict HOW TOXIC a compound is
- Thresholds for splitting are subjective
- Predictions of toxicity can always be categorized AFTER prediction

Loss of Information



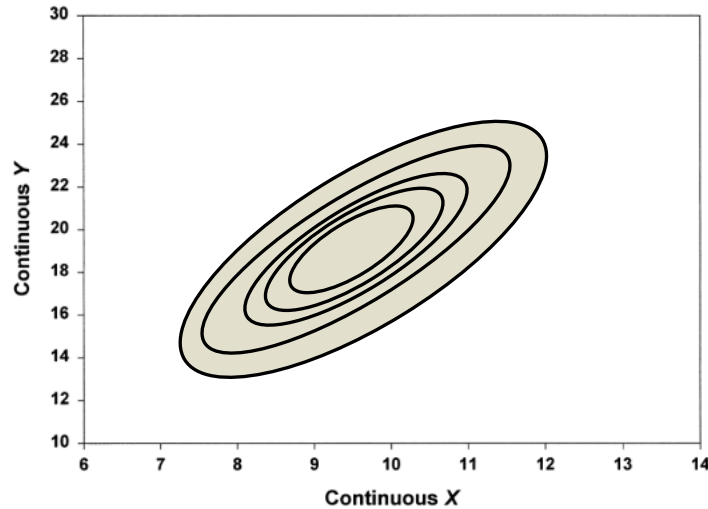
Scenario:

- C is closer to B than to D

Result:

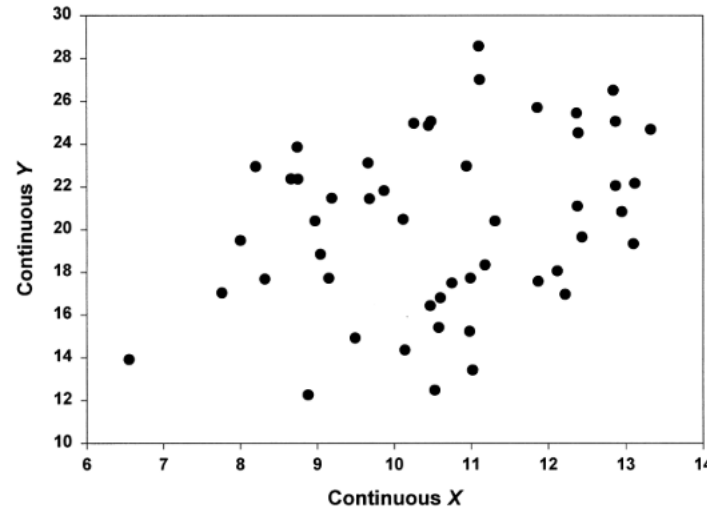
- Loss of individual differences between observations
- C and D are judged to be more similar than C and B

Loss of Effect Size and Statistical Significance



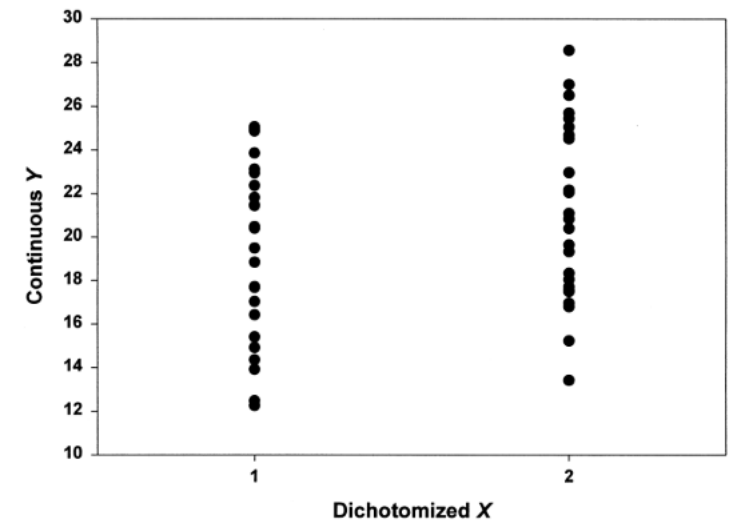
Population:

- $n = > 1 \times 10^6$
- $\rho_{xy} = 0.40$



Continuous Sample:

- $n = 50$
- $r_{xy} = 0.30$
- $95\% \text{ CI} = [0.02, 0.53]$
- *Null Hypothesis:* $\rho_{xy} = 0.0$
- $t(48) = 2.19, p = 0.03$



Dichotomized Sample:

- $n = 50$
- $r_{xy} = 0.21$
- $95\% \text{ CI} = [-0.07, 0.46]$
- *Null Hypothesis:* $\mu_1 = \mu_2$
- $t(48) = 1.47, p = 0.15$

Splitting Up: It's a Bad Idea..

STATISTICS IN MEDICINE
Statist. Med. 2006; **25**:127–141

Published online 11 October 2005 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/sim.2331

Psychological Methods
2002, Vol. 7, No. 1, 19–40

Copyright 2002 by the American Psychological Association, Inc.
1082-989X/02/\$5.00 DOI: 10.1037/1082-989X.7.1.19

Dichotomizing continuous predictors in multiple regression: a bad idea

Patrick Royston^{1,*†}, Douglas G. Altman² and Willi Sauerbrei³

JULIE R. IRWIN and GARY H. McCLELLAND*

Marketing researchers frequently split (dichotomize) continuous predictor variables into two groups, as with a median split, before performing data analysis. The practice is prevalent, but its effects are not well understood. In this article, the authors present historical results on the effects of dichotomization of normal predictor variables rederived in a regression context that may be more relevant to marketing researchers. The authors then present new results on the effect of dichotomizing continuous predictor variables with various nonnormal distributions and examine the effects of dichotomization on model specification and fit in multiple regression. The authors conclude that dichotomization has only negative consequences and should be avoided.

Negative Consequences of Dichotomizing Continuous Predictor Variables

Splitting a Predictor at the Upper Quarter or Third and the Lower Quarter or Third

Andrew GELMAN and David K. PARK

On the Practice of Dichotomization of Quantitative Variables

Robert C. MacCallum, Shaobo Zhang, Kristopher J. Preacher, and Derek D. Rucker
Ohio State University

described, and justifications that are offered for such usage are examined. The authors present the case that dichotomization is rarely defensible and often will yield misleading results.

Dichotomizing Continuous Outcome Variables: Dependence of the Magnitude of Association and Statistical Power on the Cutpoint

David R. Ragland

Dichotomizing a continuous outcome variable casts that variable in traditional epidemiologic terms (that is, disease, no disease). One consequence is overall reduced statistical power. A more fundamental concern is that the magnitude

Finding What Is Not There through the Unfortunate Binning of Results: The Mendel Effect

Howard Wainer, Marc Gessaroli, and Monica Verdi
National Board of Medical Examiners

uniformly or normally distributed. By discretizing x into three categories, we claw back about half the efficiency lost by the commonly used strategy of dichotomizing the predictor.

Strategy

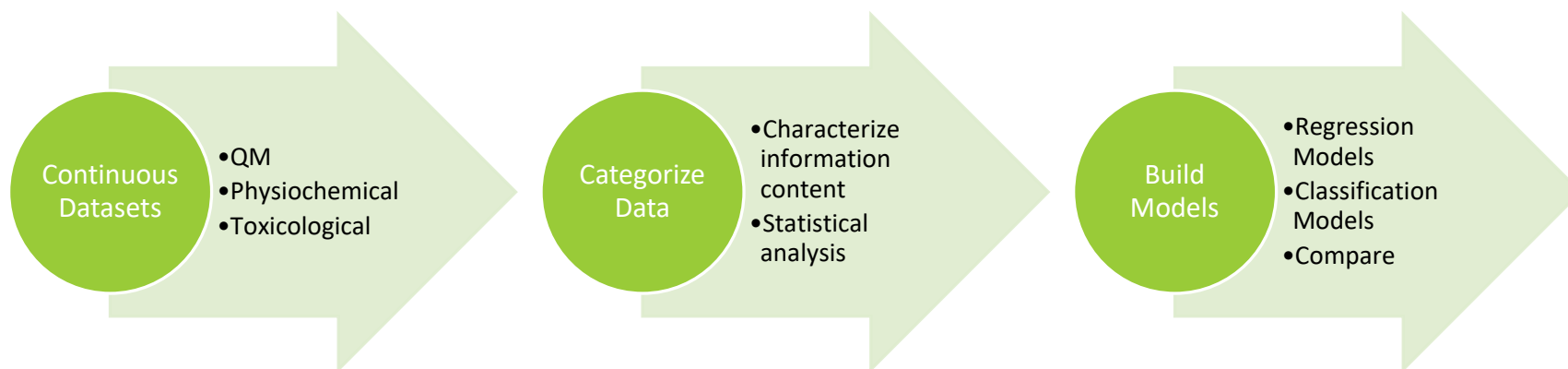
Hypothesis

Categorization of continuous data is bad statistical practice
and distorts the relationship between variables.

Will this fundamental principle result in less predictive machine learning models?
How does categorization affect the prediction accuracy?

Approach

Using continuous datasets, make predictions *before* (Regression) and *after* (Classification) categorization.



Datasets

Dataset	Category	Number of Molecules ^a	Endpoint	Range
G298_atom ¹	Quantum Mechanical	131,082	$\Delta G^\circ_{\text{at}}$ (kcal mol ⁻¹)	-2,417 – -288
Solv	Physiochemical	642	$\Delta G^\circ_{\text{hyd}}$ (kcal mol ⁻¹)	-25.5 – 3.4
Tox_102 ^{b,2}	Toxicological <i>in vitro</i>	971	logAC ₅₀	-2.1 – 4.7
Tox_134 ^{c,2}	Toxicological <i>in vitro</i>	1,347	logAC ₅₀	-4.0 – 2.8

^a Original size of the dataset. If datasets have more than 1,000 molecules, they were randomly sampled down to a size of 1,000 before modeling.

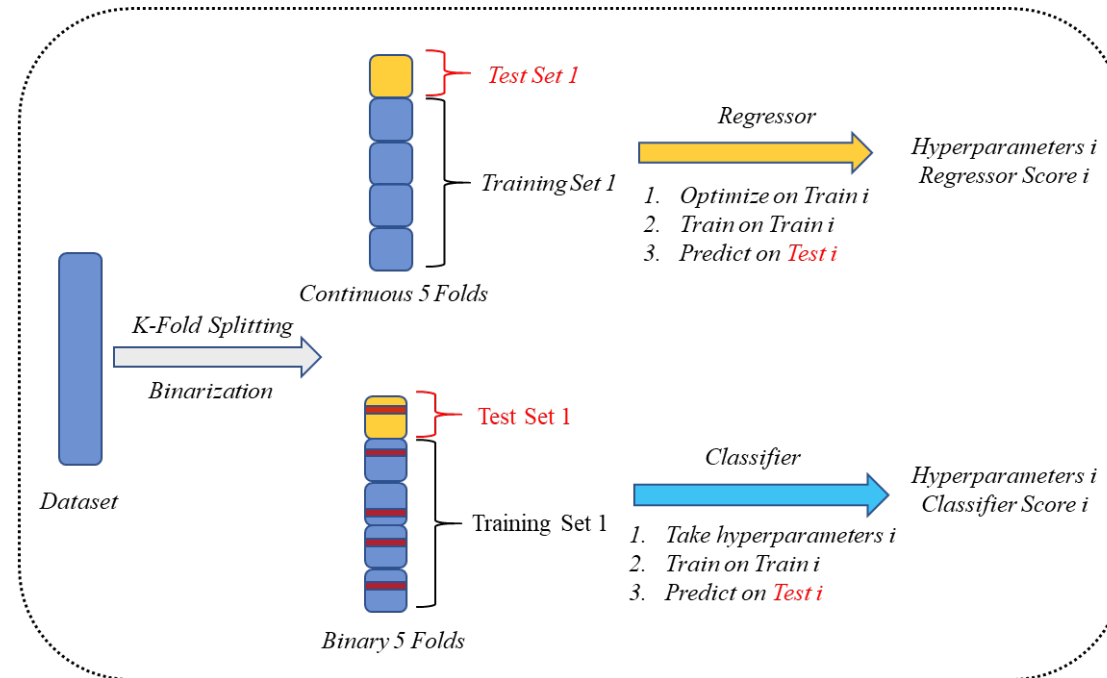
^b Includes data exclusively from the ATG-PPre-cis assay

^c Includes data exclusively from the ATG-PPARg-trans assay

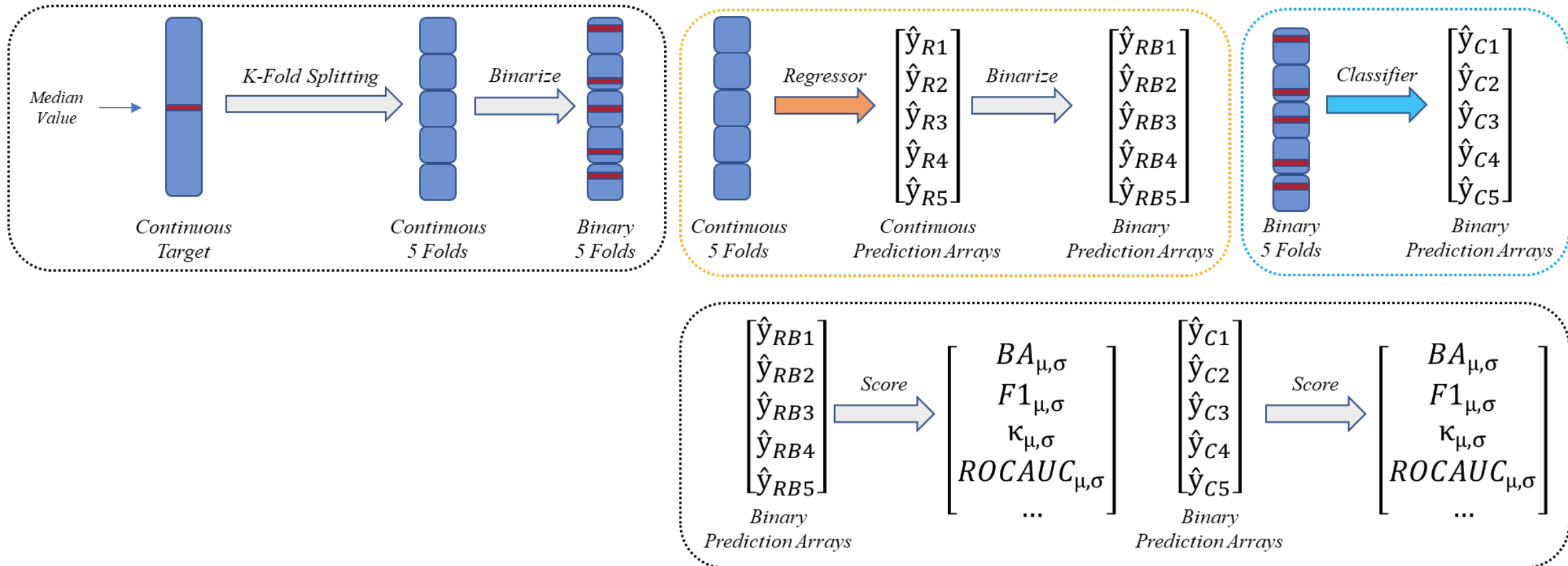
Algorithms and Hyperparameters

Algorithm	Hyperparameters Searched in Optimization ^{a,b}
Decision Tree (DT)	<i>max depth</i> $\in (50, 100, 200, 500)$ <i>min samples split</i> $\in (2, 5, 10, 20, 40)$ <i>min samples leaf</i> $\in (1, 5, 10, 20)$
k- Nearest Neighbors (kNN)	<i>k</i> $\in (2, 3, \dots, 22)$
Random Forest (RF)	<i>n estimators</i> $\in (10, 25, 50, 100, 150, 200)$ <i>max depth</i> $\in (50, 100, 200, 500)$ <i>min samples split</i> $\in (2, 5, 10, 20, 40)$ <i>min samples leaf</i> $\in (1, 5, 10, 20)$
Support Vector Machines (SVM)	<i>kernel</i> : RBF, Sigmoid <i>C</i> $\in (0.001, 0.01, 0.1, 1, 10)$
Deep Neural Network (DNN)	<i>N hidden layers</i> $\in (2, 3, 4, 5, 6, 7, 8)$ <i>N hidden units per layer</i> $\in (32, 64, 128)$ <i>Regularizer</i> : L1, L2, No regularizer <i>Output layer bias</i> : True or False <i>Class weighting</i> : True or False

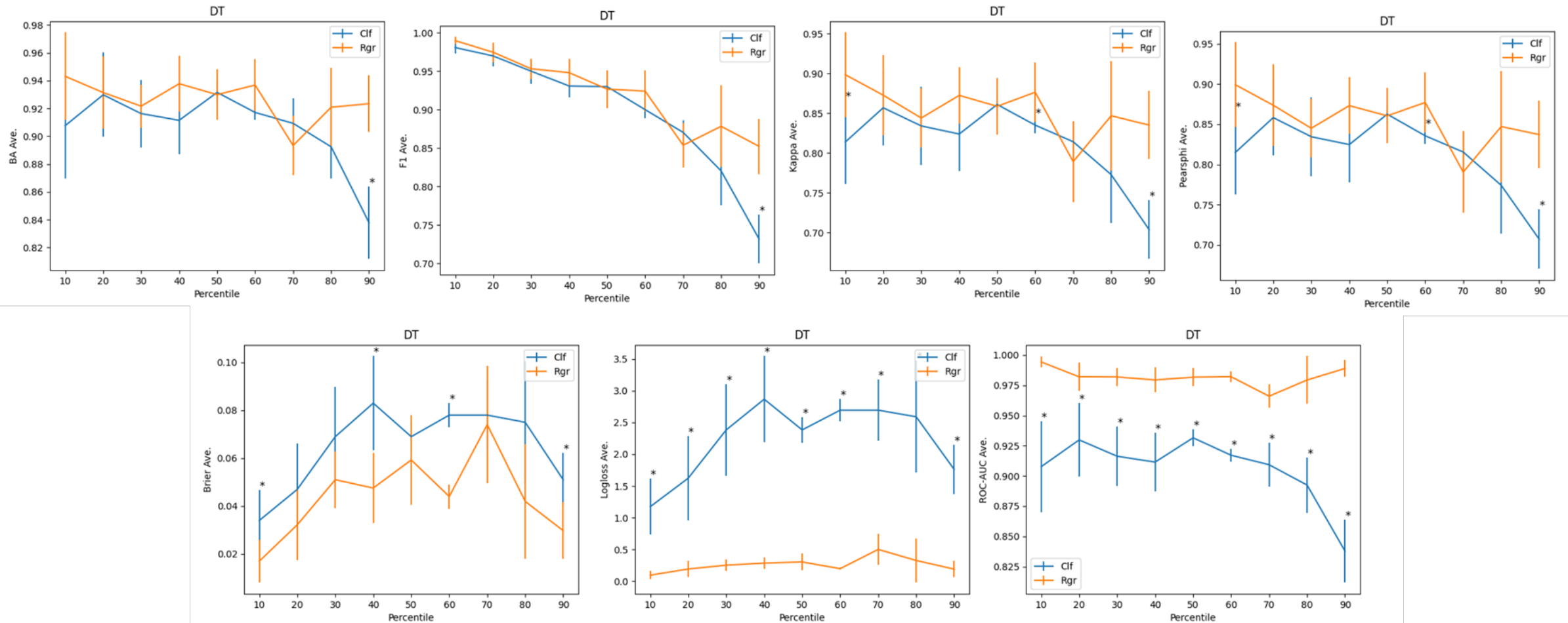
Hyperparameter optimization



Comparing Classification and Regression



G298Atom - DT



* Statistical significance of difference of means determined by independent T-test with equal variances

G298Atom

Each cell is for splitting at the 50th percentile; **orange**: regressor has higher score, **blue**: classifier has higher score, **white**: statistically insignificant difference

1000

G298atom	DT	kNN	RF	SVM
BA				
F1				
Kappa				
Pearsphi			blue	
Brier				
Logloss	orange			
ROC-AUC	orange		blue	

1000, Optimized hyperparameters

G298atom	DT	kNN	RF	SVM
BA				
F1				
Kappa				
Pearsphi				
Brier				blue
Logloss	orange		blue	blue
ROC-AUC	orange			

1000, Scaled

G298atom	DT	kNN	RF	SVM
BA				blue
F1				blue
Kappa				blue
Pearsphi				blue
Brier				blue
Logloss	orange		blue	blue
ROC-AUC	orange		blue	blue

1000, Scaled, CorrFilt60

G298atom	DT	kNN	RF	SVM
BA	orange			blue
F1	orange			blue
Kappa	orange			blue
Pearsphi	orange			blue
Brier	orange			blue
Logloss	orange	orange		blue
ROC-AUC	orange	orange	blue	blue

1000, Scaled, VarFilt25, CorrFilt60

G298atom	DT	kNN	RF	SVM
BA	orange			blue
F1				blue
Kappa	orange			blue
Pearsphi	orange		blue	blue
Brier	orange			blue
Logloss	orange	orange		blue
ROC-AUC	orange		blue	blue

1000, Scaled, VarFilt25, CorrFilt95, Optimized

G298atom	DT	kNN	RF	SVM
BA				orange
F1				orange
Kappa				orange
Pearsphi				orange
Brier				
Logloss	orange			
ROC-AUC	orange	orange		

DNN Results

Each cell represents the results for splitting data at the 50th percentile

No Regularization

G298atom/	32*2	32*8	64*2	64*8	128*2	128*8
BA						
F1						
Kappa						
PearsPhi						
Brier						
Logloss						
ROC-AUC						

L1 Regularization

G298atom/	32*2	32*8	64*2	64*8	128*2	128*8
BA						
F1						
Kappa						
PearsPhi						
Brier						
Logloss						
ROC-AUC						

L2 Regularization

G298atom/	32*2	32*8	64*2	64*8	128*2	128*8
BA						
F1						
Kappa						
PearsPhi						
Brier						
Logloss						
ROC-AUC						

DNN Results

Using an architecture with 8 hidden layers and 128 nodes per layer, the class weighting and output bias of the DNN classifiers were turned on and off

L1 Regularization

G298atom/	Output/Class	No/Class	Output/No	No/No
BA				
F1				
Kappa				
PearsPhi				
Brier				
Logloss				
ROC-AUC				

L2 Regularization

G298atom/128*8	Output/Class	No/Class	Output/No	No/No
BA				
F1				
Kappa				
PearsPhi				
Brier				
Logloss				
ROC-AUC				

Conclusions

Approach

- Categorization of continuous data is bad statistical practice. But does it affect the predictivity of models?
- By making predictions *before (regression)* and *after (classification)* categorizing a continuous dataset, we can explore how categorization affects model performance

Results

- There are observable differences in model performance when continuous data is categorized
- Relative performance is dependent on cutpoint, algorithm, and dataset
- *Probabilistic metrics* are sometimes needed to distinguish performance
- *Optimization, variance filtering, and correlation filtering* change the relative performance
- The relative performance of DNN regressors and classifiers have some dependence on network architecture and regularization

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Mentors



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Tox102 and Tox134 Datasets

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Thank You!
Q & A