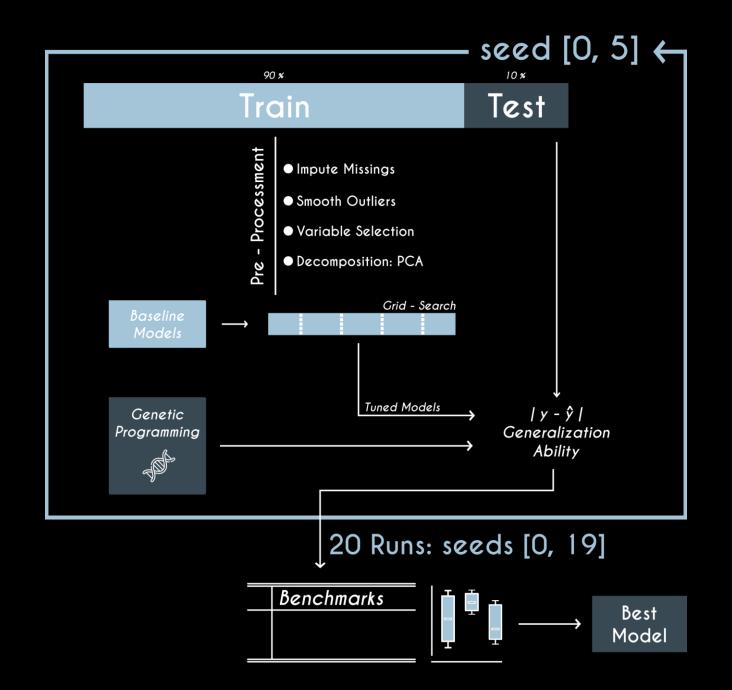
CHILDREN'S ALCOHOL CONSUMPTION

Machine Learning

Data Science and Advanced Analytics

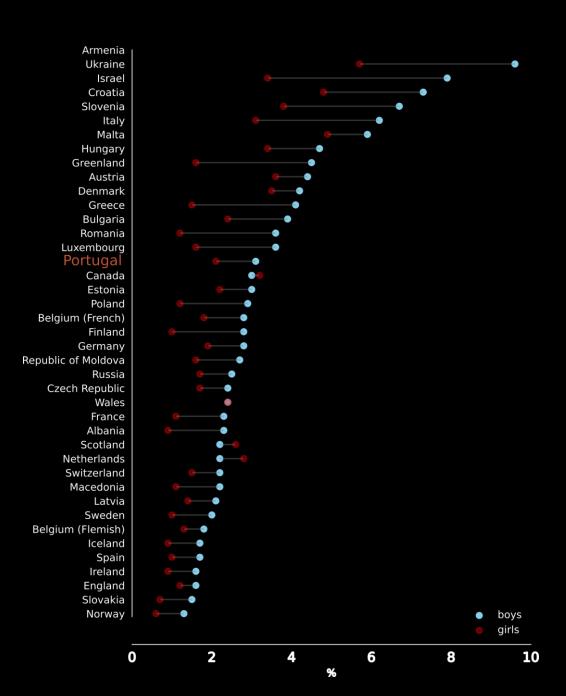
Rita Franco m20180080 Rodrigo Umbelino m20180060 Vitor Manita m20180054

Process



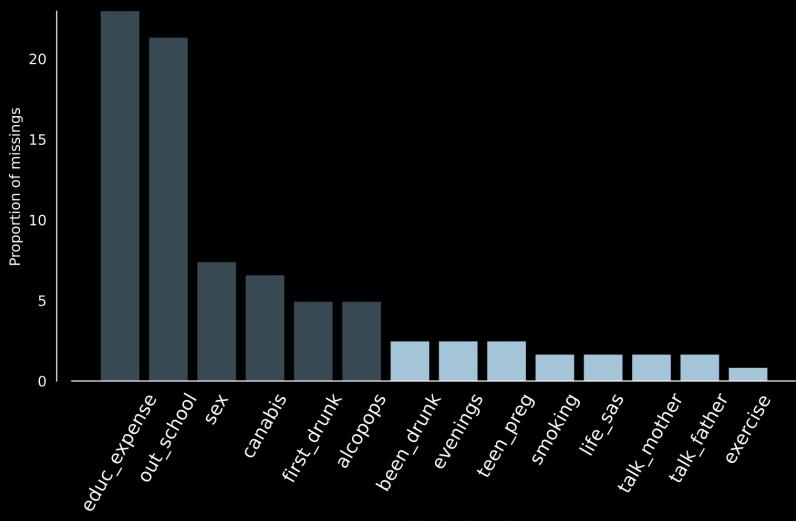
Explore

Portugal is the 15th country where boys claim they drink more often



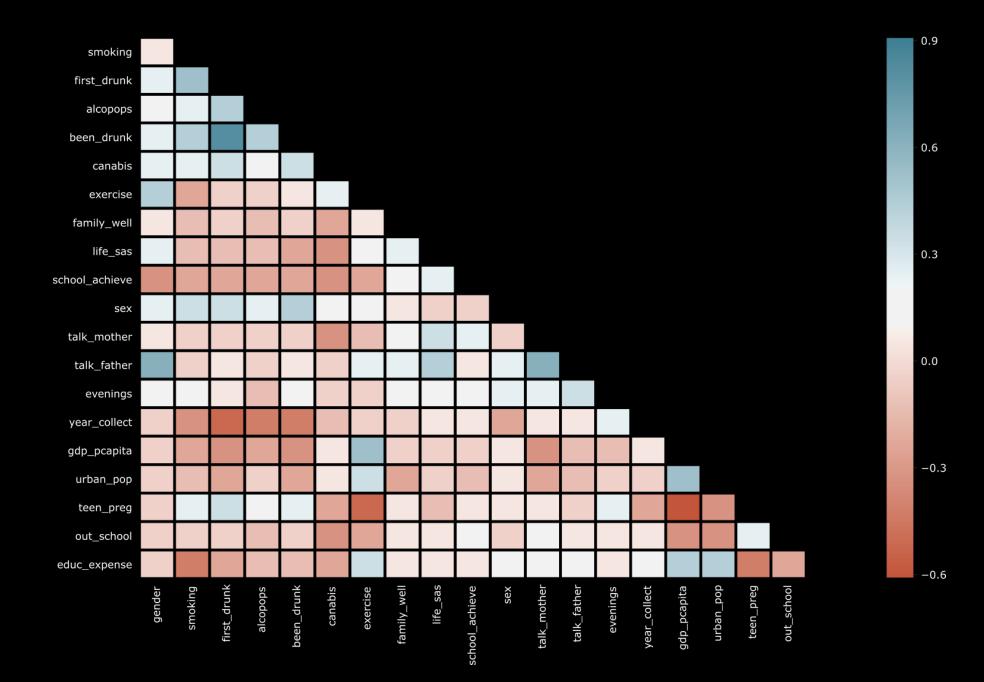
Explore

3% cutoff line on missing values



Features with missing values

Explore



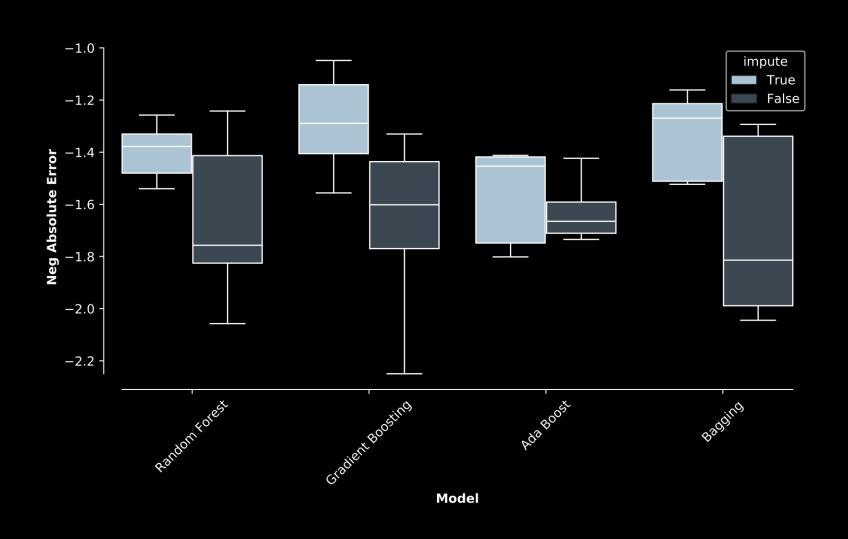
Modify

Our strategy

Impute Missings

{(T/F), (T/F), (T/F), (T/F)}

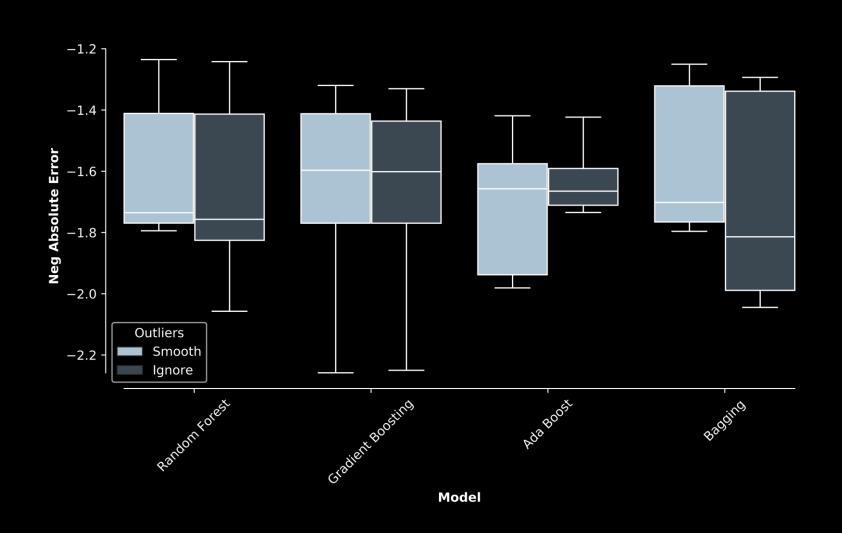
Using the distribution of each feature, fill missings by mean or median



Smooth Outliers

{(T/F), (T/F), (T/F), (T/F)}

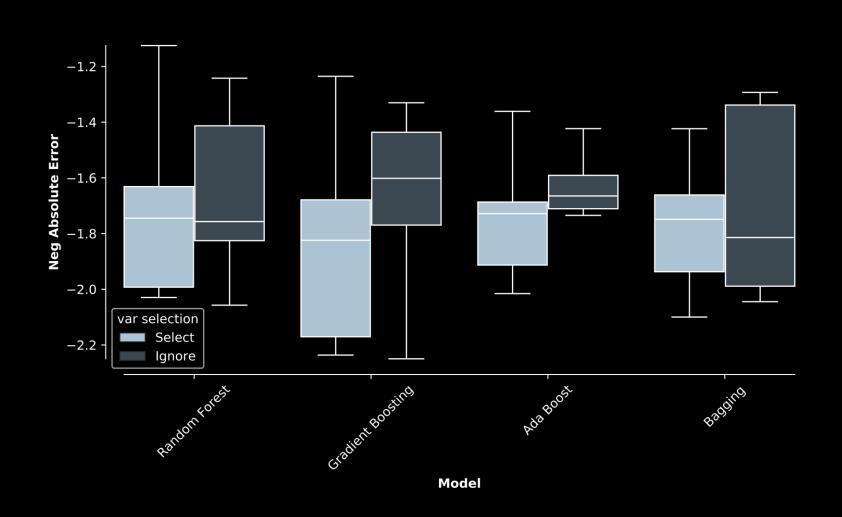
Using winsoring with percentiles 5% and 95%



Variable Selection

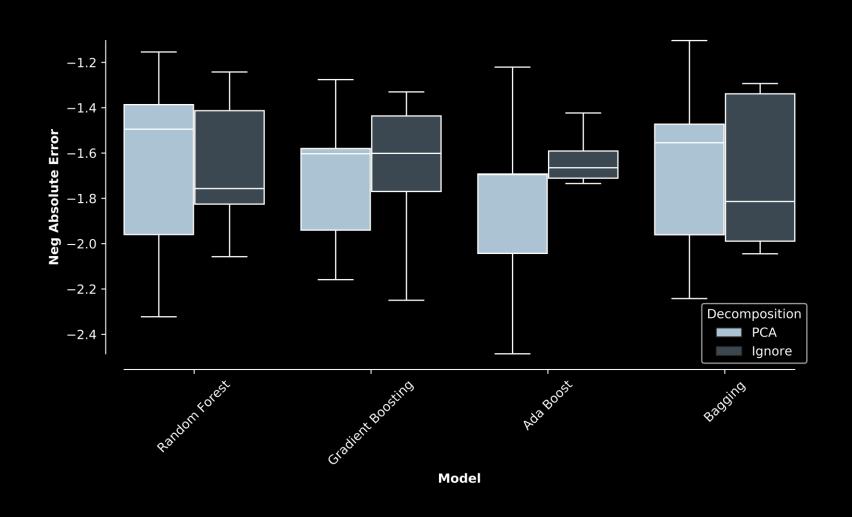
{(T/F), (T/F), (T/F), (T/F)}

Using Recursive Feature Extraction with Linear Regression



Feature Decomposition {(T/F), (T/F), (T/F)}

Using Principal Component Analysis. Automatic Threshold of 80% explained variance



Ensembles Benchmarks

	Model	lmpute Missings	Smooth Outliers	Variable Selection	PCA	NMAE	MAE std
5 sls	Gradient Boost	True	True	False	False	-1.286	0.183
	Gradient Boost	True	False	False	False	-1.286	0.182
est	Gradient Boost	True	False	True	False	-1.286	0.182
m Z	Bagging	True	False	True	False	-1.320	0.160
	Gradient Boost	True	True	False	False	-1.330	0.160
	Bagging	False	True	True	True	-1.963	0.377
t 5 els	Random Forest	False	True	True	True	-1.845	0.317
Worst Model	Gradient Boost	False	True	True	True	-1.842	0.346
	Bagging	True	True	True	True	-1.838	0.374
	Gradient Boost	False	False	True	False	-1.829	0.363

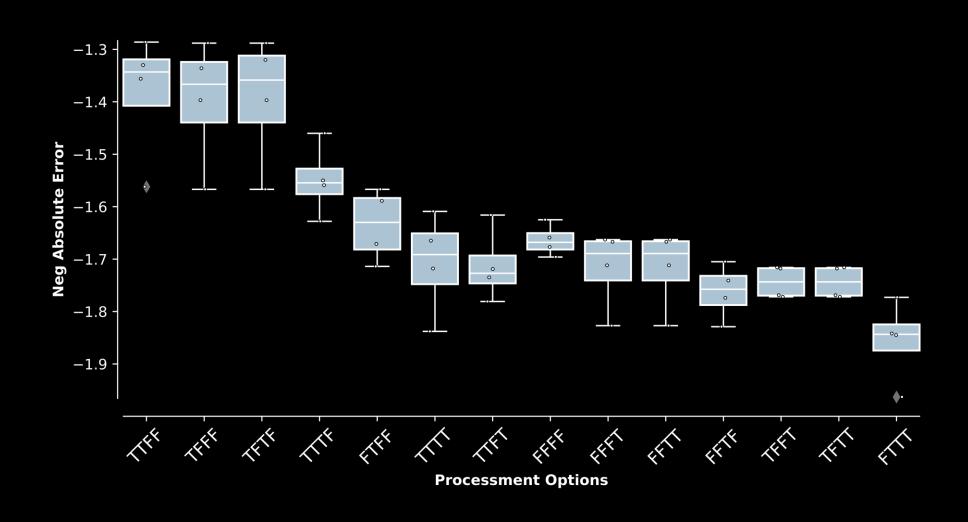
Grid Search in each model with 5 cross validations was performed

Ensembles Benchmarks

	Model	Impute Missings	Smooth Outliers	Variable Selection	PCA	NMAE	MAE std
	Gradient Boost	True	True	False	False	-1.286	0.183
2 2	Gradient Boost	True	False	False	False	-1.286	0.182
Best Mode	Gradient Boost	True	False	True	False	-1.286	0.182
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Ensembles Benchmarks

{T, T, F, F}



1. Generate K Clusters (K-means)

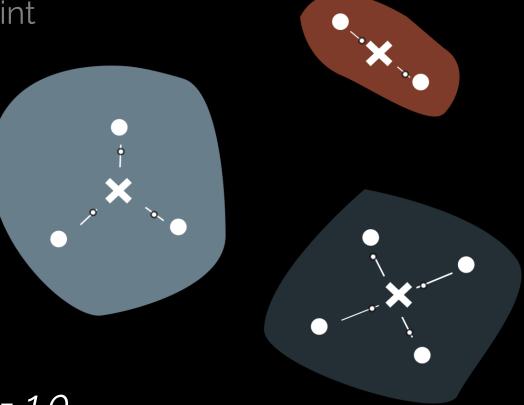
- 1. Generate K Clusters (K-means)
- 2. Generate random coordinates between centroids and each corresponding point



1. Generate K Clusters (K-means)

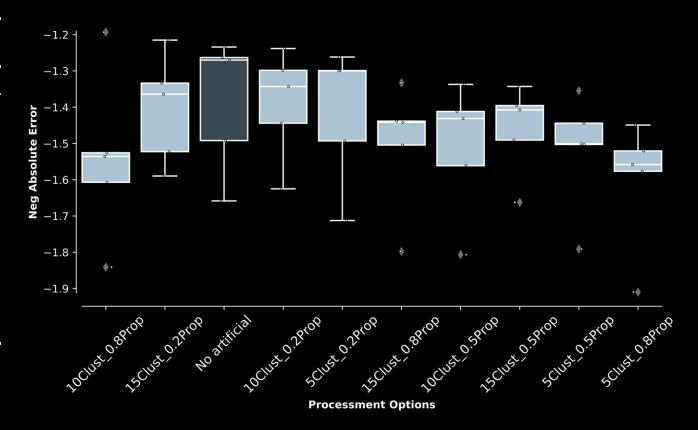
2. Generate random coordinates between centroids and each corresponding point

3. Generate p proportion of new data



P (proportion) = 1.0

	Nr. Clusters	Increase Proportion	NMAE
No Artificial	O	0	-1.383
	10	20%	-1.390
	15	20%	-1.405
	5	20%	-1.413
	15	50%	-1.460
Artificial	15	80%	-1.503
	10	50%	-1.510
	5	50%	-1.519
	10	80%	-1.540
	5	80%	-1.603



	Nr. Clusters	Increase Proportion	NMAE
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Genetic Programming

Selection

Roulette Wheel Stochastic Universal Sampling Random Bloat Control Rank

Genetic Programming

Selection

Roulette Wheel Stochastic Universal Sampling Random Bloat Control Rank

Crossover

Uniform
Simple
2 Tree Crossover

Genetic Programming

Selection

Roulette Wheel Stochastic Universal Sampling Random Bloat Control Rank

Crossover

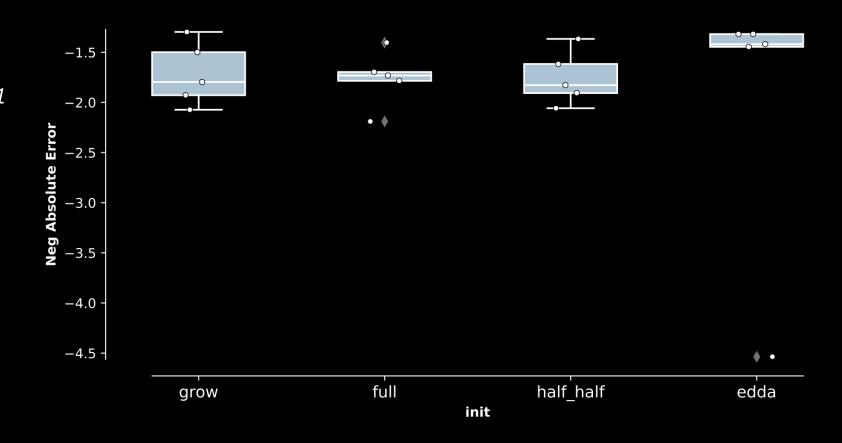
Uniform
Simple
2 Tree Crossover

Mutation

Reverse Shake Graft Swap Semantical Sig

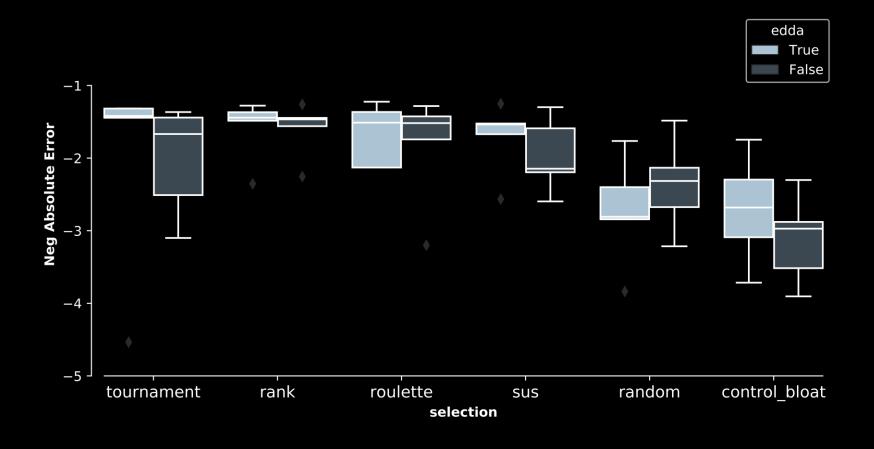
Initialization

200 Generations 200 Population size Parsimony Coefficient = 0.001



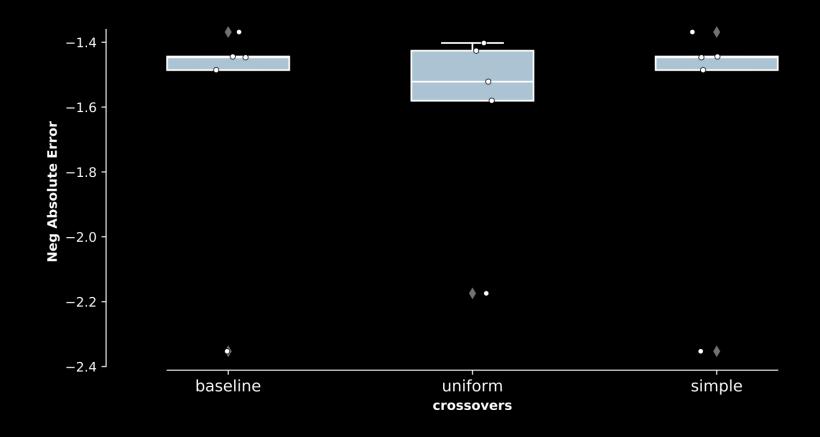
Selection

Effect of Edda on generalization ability dispersion is visible



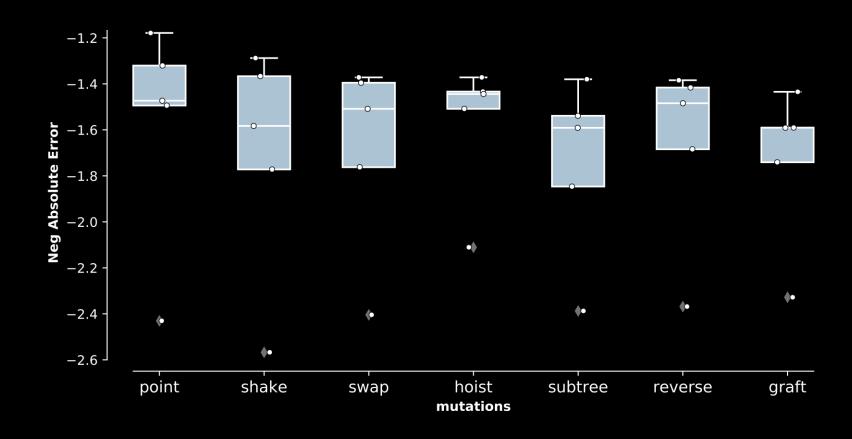
Crossover

Prob. Crossover = 0.9 Prob. Mutation = 0.1



Mutation

Prob. Crossover = 0.1 Prob. Mutation = 0.9

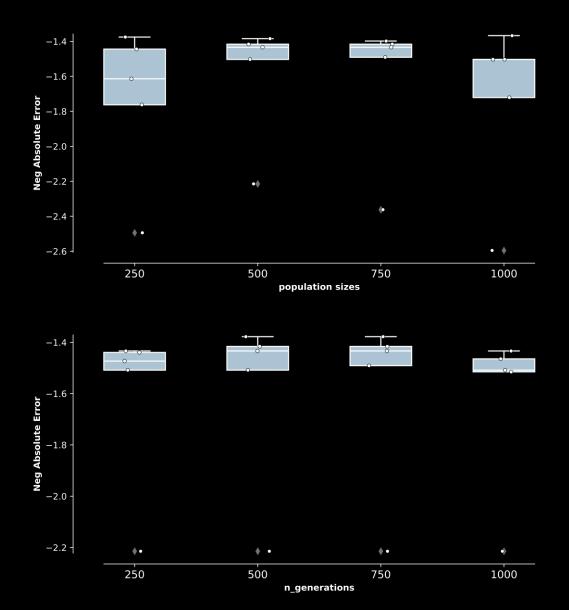


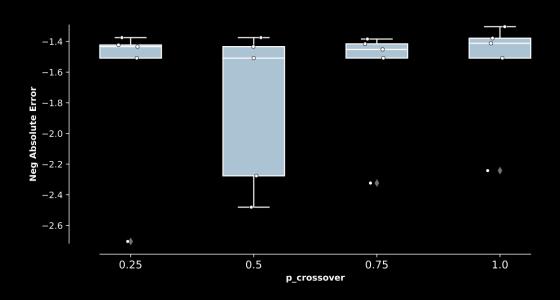
GP - Deeper into the parameters

From the previous benchmarks we now use:

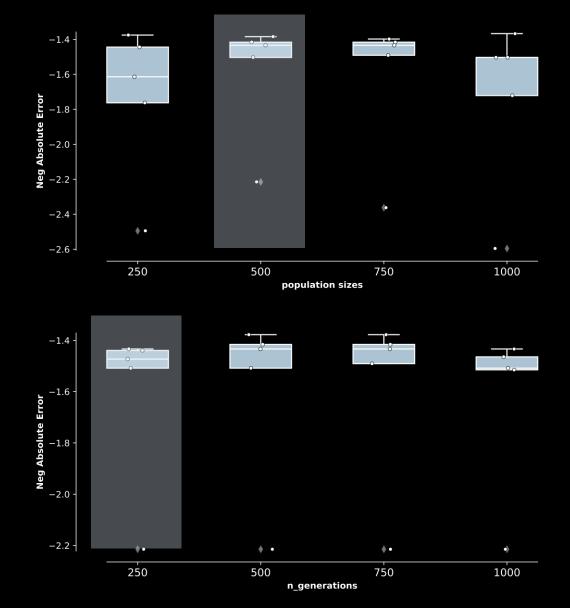
- Edda initialization
- Rank selector
- Baseline Crossover
- Hoist mutation

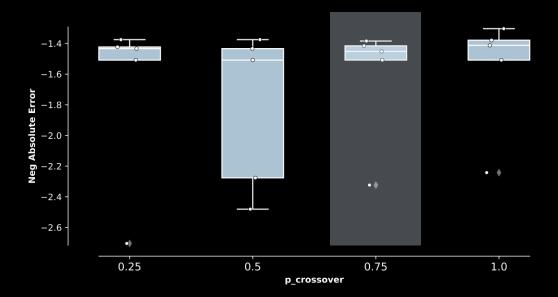
GP - Deeper into the parameters



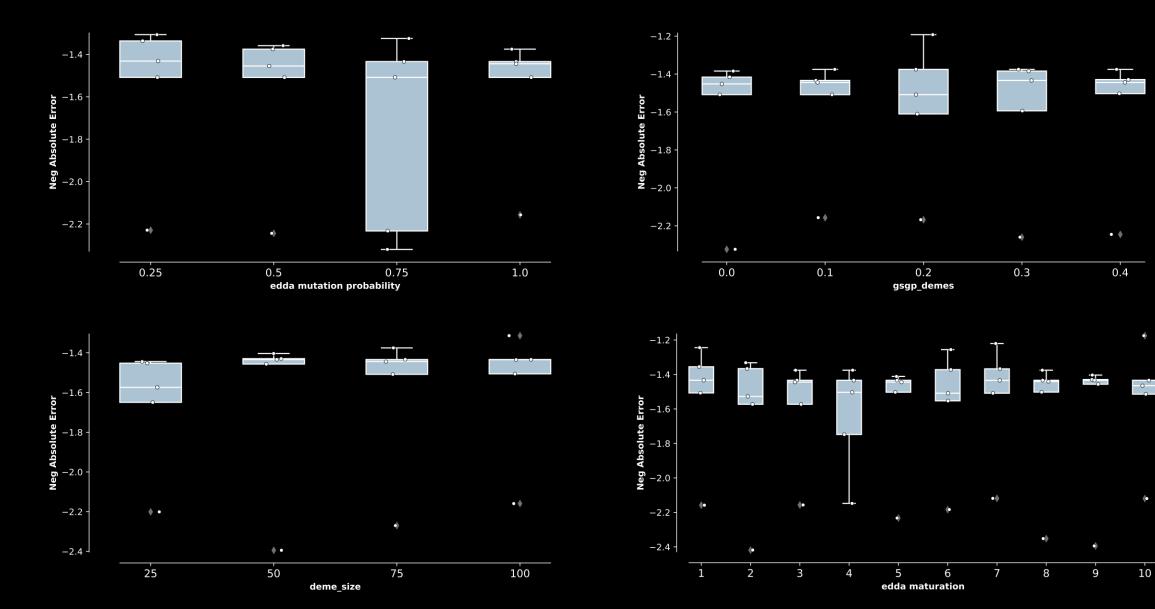


GP - Deeper into the parameters

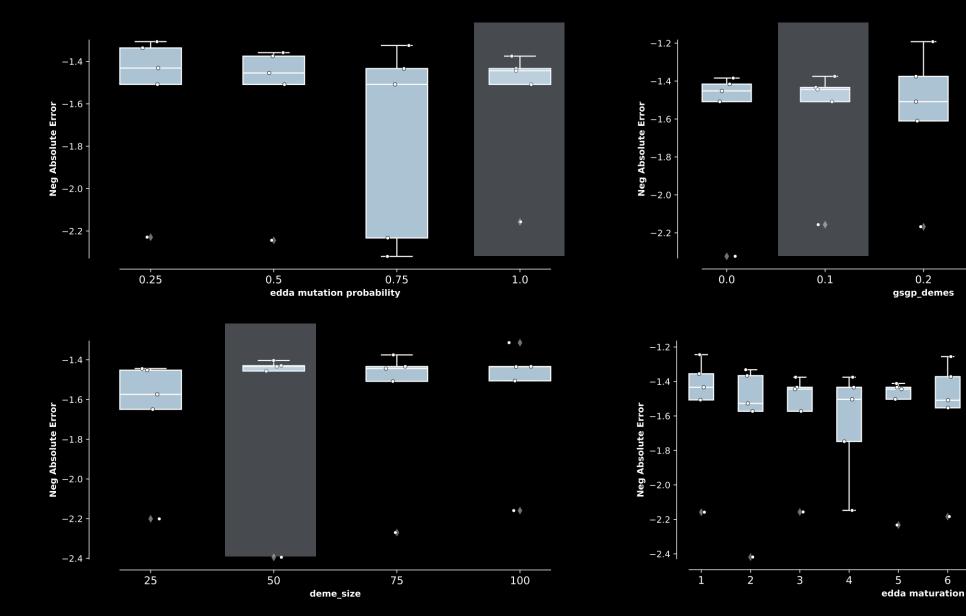




GP - Edda params



GP - Edda params



• •

0.4

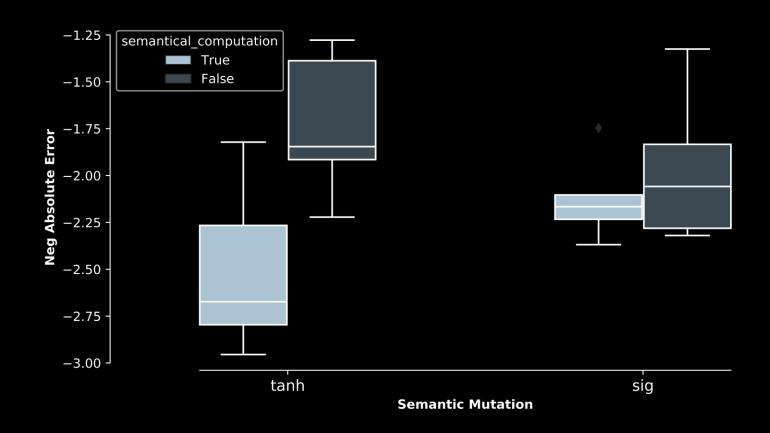
10

9

0.3

GP - Semantic Operatos

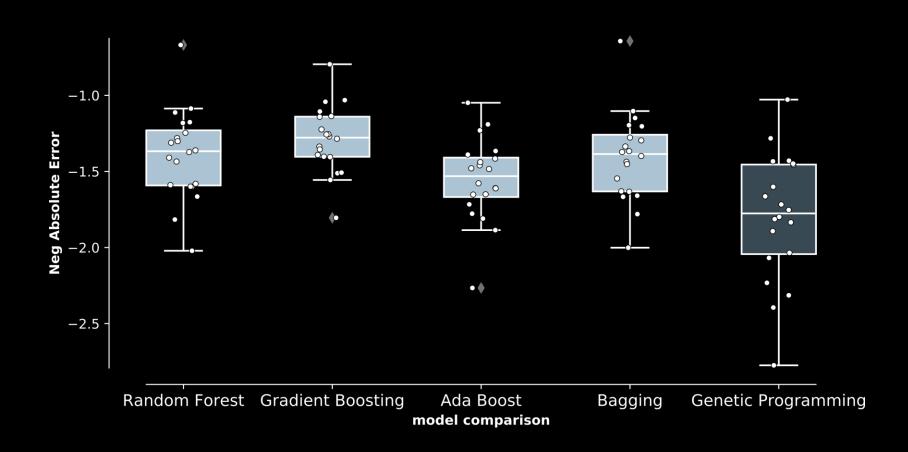
Due to some problems, generation and population sizes were set to 20



Comparing Ensembles to GP

Can genetic programming performance be worse than a simpler model?

Lets test it 20 times



Comparing Ensembles to GP

	Model	NMAE
Ensembles	Gradient Boosting	-1.291
	Random Forest	-0.391
	Bagging	-1.407
	Ada Boost	-1.553
GP	Genetic Programming	-1.799

Comparing Ensembles to GP

	Model	NMAE
Ensembles	Gradient Boosting	-1.291
	Random Forest	-0.391
	Bagging	-1.407
	Ada Boost	-1.553
СР	Genetic Programming	-1.799

t-test

t = 4.79 p-value = 0.003%

Means are statistically different for usual confidence levels of 1%, 5% and 10%

Conclusions

Hard Data collection

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Lack of extensive online support on this subject made the process of implementing new things more extensive and time consuming

Conclusions

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Unexpected Results

We really did not expect Gradient Boost to outperform a complex algorithm like Genetic Programming. Outcome may be a result of the data or the preprocessing choices made.

Thank you

