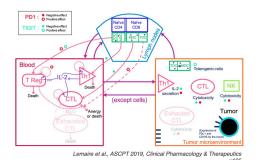
Key Objectives: ML Analysis

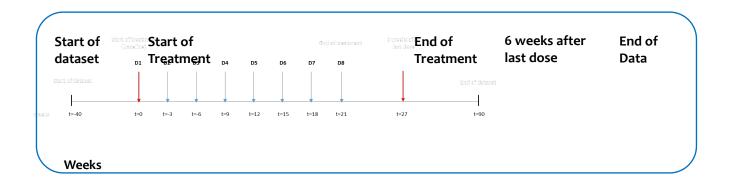
- Using the 144 QSP Parameters, is it possible to build a Machine Learning Model to predict the Categorical response(Classification)?
- For the top models what are the most influential parameters for each Task?



"Biology is likely far too complex and messy to ever be encapsulated as a simple set of neat mathematical equations. But just as mathematics turned out to be the right description language for physics, biology may turn out to be the perfect type of regime for the application of Al."

- Demis Hassabis, CEO: DeepMind/Isomorphic Labs

Introduction: Dosing Description



Untreated case and 3 treatment arms:

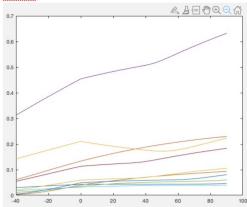
- ☐ Untreated
- ☐ Atezolizumab

- 1. T: Tumor size (pmol tumor cells)
- 2. Ag: Tumor antigens in the tumor space (pmol tumor antigens per liter of tumor space)
- 3. R: T Regulatory cells in peripheral blood (pmol cells)
- 4. H: T helper 1 cells in peripheral blood (pmol cells)
- 5. C: Cytotoxic T cells in peripheral blood (pmol cells)
- 6. RT: T Regs in the tumor space (pmol cells)
- 7. HT: T helper 1 cells in the tumor space (pmol cells)
- 8. CT: Cytotoxic T cells int the tumor space (pmol cells)
- Cyde: Total cytotoxic death (total pmol tumor cells killed per liter of tumor space per day)

Output Variables

- 1. T: Tumor size (pmol tumor cells)
- 2. Ag: Tumor antigens in the tumor space (pmol tumor antigens per liter of tumor space)
- 3. R: T Regulatory cells in peripheral blood (pmol cells)
- 4. H: T helper 1 cells in peripheral blood (pmol cells)
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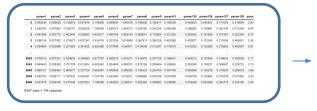
Plots the tumor curves of 10 VPs drawn randomly from the VPop after treatment with atezolizumab:





Tumor Response Predictions

ODE parameter input (nVP x Parameter Total)



Tumor VP Variability



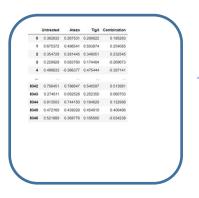
Response(Continuous)

	Untreated	Atezo	Tigit	Combination
0	0.362832	0.267531	0.289822	0.185283
1	0.675372	0.486541	0.593874	0.254085
2	0.354729	0.281445	0.349051	0.232545
3	0.229928	0.083760	0.174484	-0.269673
4	0.496833	-0.366377	0.475444	-0.397141
8342	0.756451	0.786647	0.540587	0.513981
8343	0.274611	0.092528	0.252350	0.060703
8344	0.813503	0.744150	0.184829	0.132998
8345	0.472169	0.439028	0.454819	0.406486
8346	0.521889	0.368776	0.165900	-0.034238

nVP ≡ Number of Virtual Patients

Tumor size at week o and 27

Response(Continuous)



Conditions logic

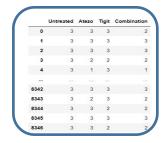
Complete Responser(Condition o)
$$\equiv \frac{T|t=27 - T|t=0}{T|t=0} = -1$$

Partial Responser(Condition 1)
$$\equiv -1 < \frac{T|t=27 - T|t=0}{T|t=0} < = -0.3$$

Stable Disease(Condition 2)
$$\equiv -0.3 < \frac{T|t=27 - T|t=0}{T|t=0} < = 0.2$$

Progressive Disease(Condition 3)
$$\equiv 0.2 < \frac{T|t=27 - T|t=0}{T|t=0}$$

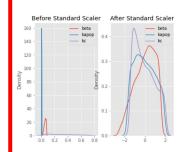
Response Type(Categorical) (nVP x Treatment Total)



Feature Scaling: Normalization

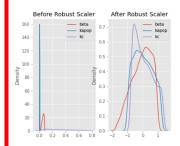
Standard Scaler

 $\frac{x_i - mean(x)}{stdev(x)}$



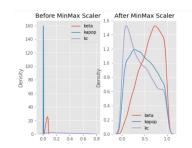
Robust Scaler

$$\frac{x_i - Q_1(x)}{Q_3(x) - Q_1(x)}$$



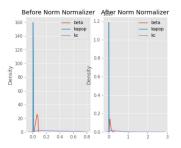
$\begin{array}{c} \mathsf{MinMax} \\ \mathsf{Scaler} \\ {}_{x_i-min(x)} \end{array}$

 $\frac{x_i - min(x)}{max(x) - min(x)}$



Normalizer

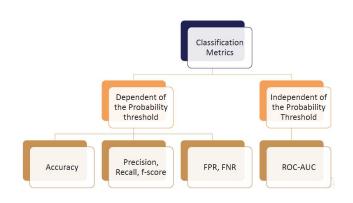
$$\overline{\sqrt{x_i^2+y_i^2+z_i^2}}$$



Hyperparameter Tuning Description

- Manual Search: Time Consuming/does not scale.
- **Grid Search:** Examines all combinations of hyperparameters. Is often called the brute force approach. Computationally Expensive, so it cannot explore entire hyperparameter space.
- Random Search: Examines hyperparameters by randomly picking a set and training the models. Less computationally expensive, but it does not learn from its past and does not guaranteed an optimal solution.
- Bayesian Optimization: It considers the set of possibilities via a Probability density function. Sequential Model Based Global Optimization using Hypeopt and Optuna was used. Average metric cross validation was minimized.
 - Random Forest
 - II. Tree-structured Parzen Estimator: Utilizes acquisition functions i.e expected improvement/bayes theorem
 - III. Gaussian Process

Model Performance Evaluations for Classification



Accuracy—	TP	+	TN
Accuracy=	\overline{P}	+	N

$$Precision = \frac{TP}{TP + FP}$$

True Positive Rate (TPR)=
$$\frac{TP}{P}$$
 = Recall

$$F1Score(F1) = \frac{2.Precision.Recall}{(Precision + Recall)}$$

	Predicted			
	Positive	Negative		
Positive	TP	FN		
Negative	FP	TN		

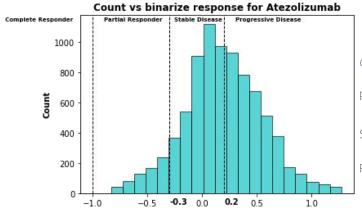
Dundistad

$$TP \equiv \text{True Positive} \mid FN \equiv \text{False Negative}$$
 $FP \equiv \text{False Positive} \mid TN \equiv \text{True Negative}$
 $P = TP + FN \equiv \text{Positives}$
 $N = FP + TN \equiv \text{Negatives}$

Other Metrics:

True Negative Rate (TNR)=
$$\frac{TN}{N}$$
 \equiv Specificity

Response Distribution Atezolizumab



Conditions logic

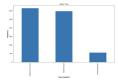
Complete Responser(Condition o)
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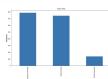
Partial Responser(Condition 1)
$$\equiv -1 < \frac{T|t=27 - T|t=0}{T|t=0} < = -0.3$$

Stable Disease(Condition 2)
$$\equiv -0.3 < \frac{T|t=27-T|t=0}{T|t=0} <= 0.2$$

Progressive Disease(Condition 3)
$$\equiv 0.2 < \frac{T|t=27 - T|t=0}{T|t=0}$$

Atezo Class Types Count/Frequencies





Key Definitions

XGBoost (Machine learning)

- Non-parametric tree-based method to predict variable of interest
- Supports use with missing data
- Amenable for binary classification, regression, and survival analyses

SHAP analysis (ML explainability)

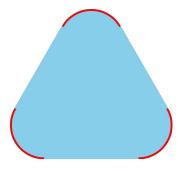
- Game theoretic approach to explain how ML models generate predictions based on inputs
- SHAP values represent the adjusted impact of an input on model prediction

Pareto Front

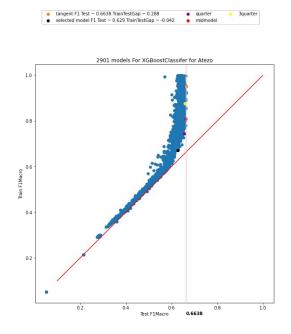
- Set of all Efficient Solutions in a multi-objective optimization set up
- Make trade-offs within the set

Convex Hull/Convex set

- Convex hull of a Shape is the smallest convex set that contains it.
- SHAP values represent the adjusted impact of an input on model prediction



Atezo; Model Selected: XGBoost with Random OverSampling



Optimal Models on Pareto Front

