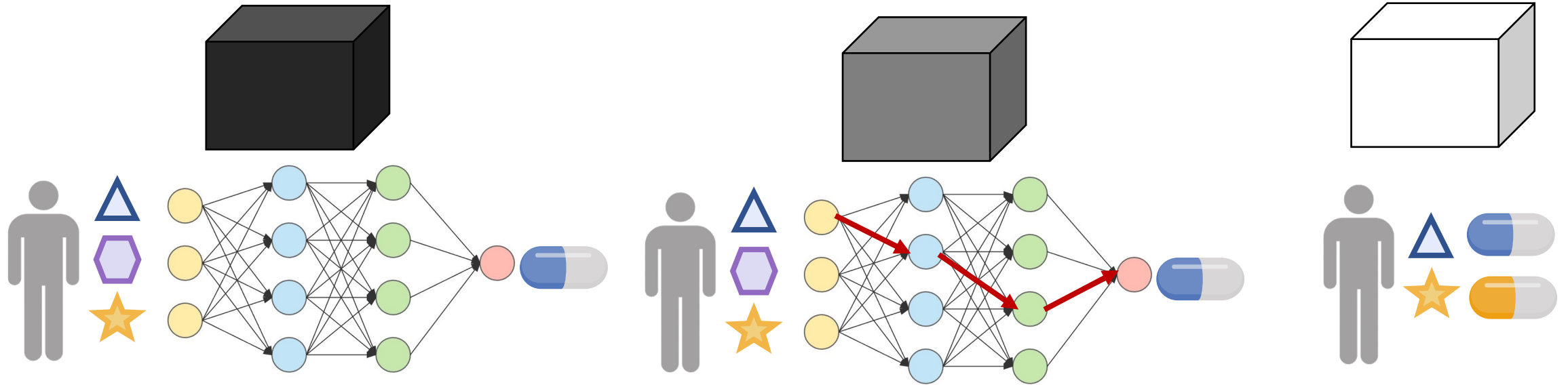


Explainable AI in Healthcare



Why Explainable AI?

- **Debugging:**
 - Unreliable and dirty data is common in real-world projects.
 - Understanding model patterns aids in identifying discrepancies with real-world knowledge, crucial for debugging.
- **Informing Feature Engineering:**
 - Feature engineering enhances model accuracy.
 - Explainable AI provides techniques to uncover important features, especially in scenarios with numerous raw features.
- **Directing Future Data Collection:**
 - Insights guide businesses in deciding what new types of data to collect.
 - Model-based insights offer an understanding of the value of existing features, aiding in the decision to collect new data.
- **Building Trust:**
 - Verification of model trustworthiness is essential.
 - Insights aligning with general understanding of the problem build trust, especially among non-experts.
- **Informing Human Decision-Making:**
 - While some decisions are automated, many crucial decisions are made by humans.
 - Model insights are valuable for human decision-makers, often more than predictions alone.

Ley de IA de la UE: primera normativa sobre
inteligencia artificial

Sociedad Actualización: 14-06-2023 - 09:38
Creado: 12-06-2023 - 11:14



Tasks in Explainable AI

- **Feature Importance**

- Identification of the most influential features in the model's predictions.
- Enables understanding which variables have a significant impact on the model's decisions.

- **Partial Dependence**

- Understanding how the model's prediction changes by varying one feature while keeping others constant.
- Aids in understanding relationships between variables and predictions.

- **Single Prediction Explanation**

- Detailed explanation of how each feature contributes to a specific prediction.
- Provides insights into the decision-making process for individual instances.

Methods


- **Provided by model design:**
 - Regression, Random Forest
- **General methods**
 - Permutation importance, SHAP

- **PDPs**

- **Provided by model design:**
 - Decision trees, Regression
- **General methods**
 - SHAP, LIME

Feature importance: Permutation importance

Height at age 20 (cm)	Height at age 10 (cm)	...	Socks owned at age 10
182	155	...	20
175	147	...	10
...
156	142	...	8
153	130	...	24



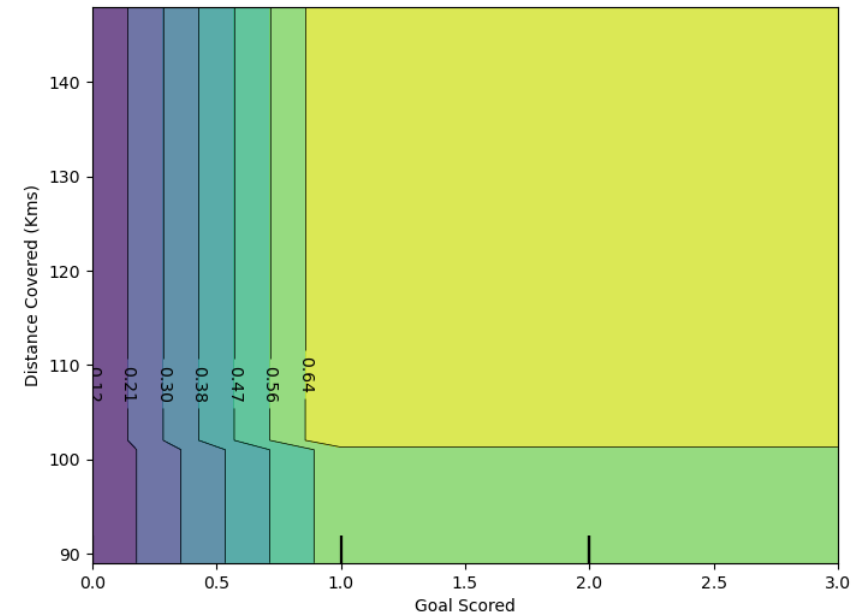
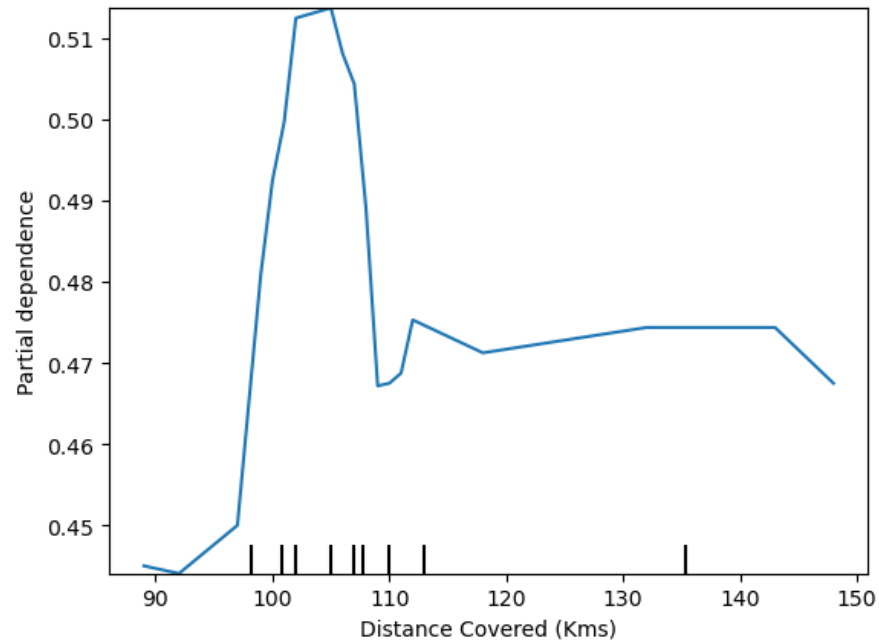
Weight	Feature
0.1750 ± 0.0848	Goal Scored
0.0500 ± 0.0637	Distance Covered (Kms)
0.0437 ± 0.0637	Yellow Card
0.0187 ± 0.0500	Off-Target
0.0187 ± 0.0637	Free Kicks
0.0187 ± 0.0637	Fouls Committed
0.0125 ± 0.0637	Pass Accuracy %
0.0125 ± 0.0306	Blocked
0.0063 ± 0.0612	Saves
0.0063 ± 0.0250	Ball Possession %
0 ± 0.0000	Red
0 ± 0.0000	Yellow & Red
0.0000 ± 0.0559	On-Target
-0.0063 ± 0.0729	Offsides
-0.0063 ± 0.0919	Corners
-0.0063 ± 0.0250	Goals in PSO
-0.0187 ± 0.0306	Attempts
-0.0500 ± 0.0637	Passes

```
# DATAI - 2023-12-13

import eli5
from eli5.sklearn import PermutationImportance

perm = PermutationImportance(my_model, random_state=1).fit(val_X, val_y)
eli5.show_weights(perm, feature_names = val_X.columns.tolist())
```

Partial Dependence Plots



```
from sklearn.inspection import PartialDependenceDisplay

# Build Random Forest model
my_model = RandomForestClassifier(random_state=0).fit(train_X, train_y)

# Plot partial dependence
disp3 = PartialDependenceDisplay.from_estimator(my_model, val_X, ['Distance Covered (Kms)'])
plt.show()
```

SHAP Values

- SHAP (SHapley Additive exPlanations) is a game theoretic approach to explain the output of any machine learning model.
- SHAP values interpret the impact of having a certain value for a given feature in comparison to the prediction we'd make if that feature took some baseline value.
- SHAP values do this in a way that guarantees a nice property. Specifically, you decompose a prediction with the following equation:

$$\text{sum}(\text{SHAP values for all features}) = \text{pred_for_team} - \text{pred_for_baseline_values}$$

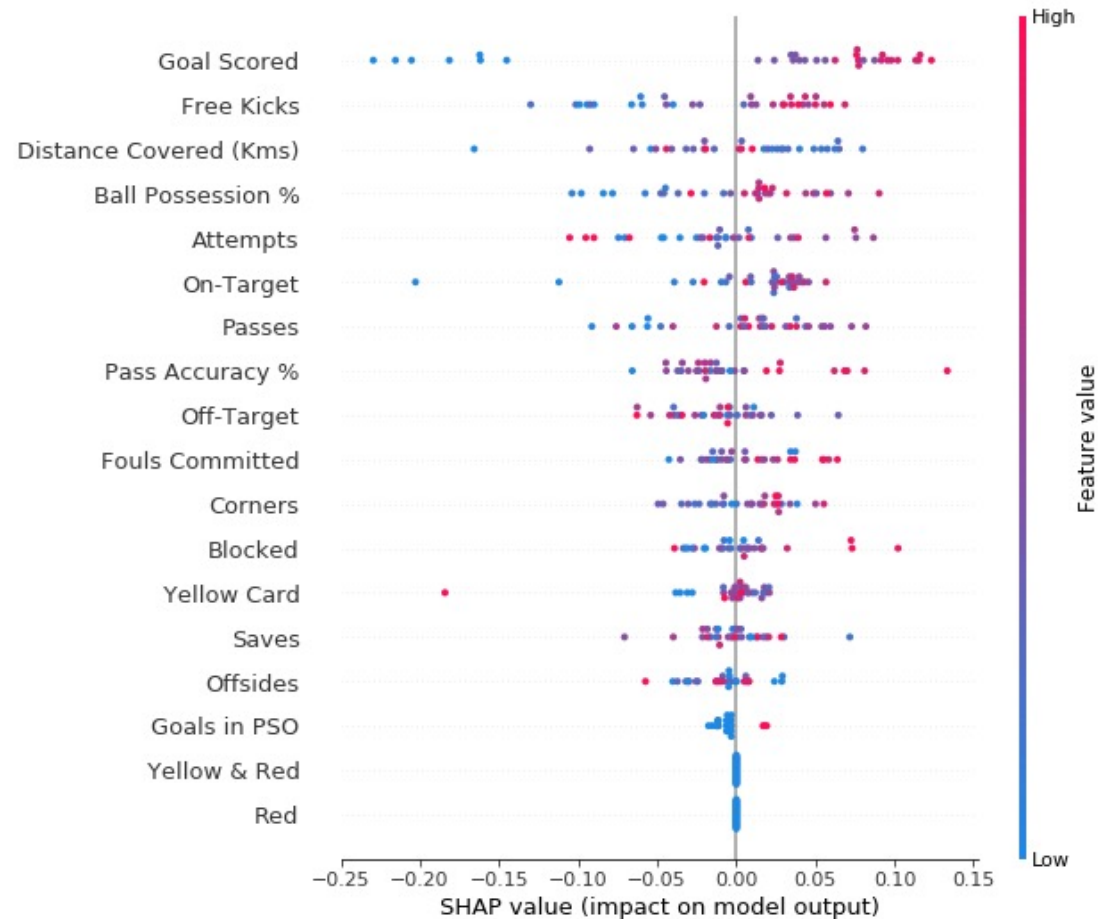
- That is, the SHAP values of all features sum up to explain why my prediction was different from the baseline. This allows us to decompose a prediction in a graph like this:



SHAP Summary Plots

```
import shap
```

```
explainer = shap.TreeExplainer(my_model)  
shap_values = explainer.shap_values(val_X)  
shap.summary_plot(shap_values[1], val_X)
```

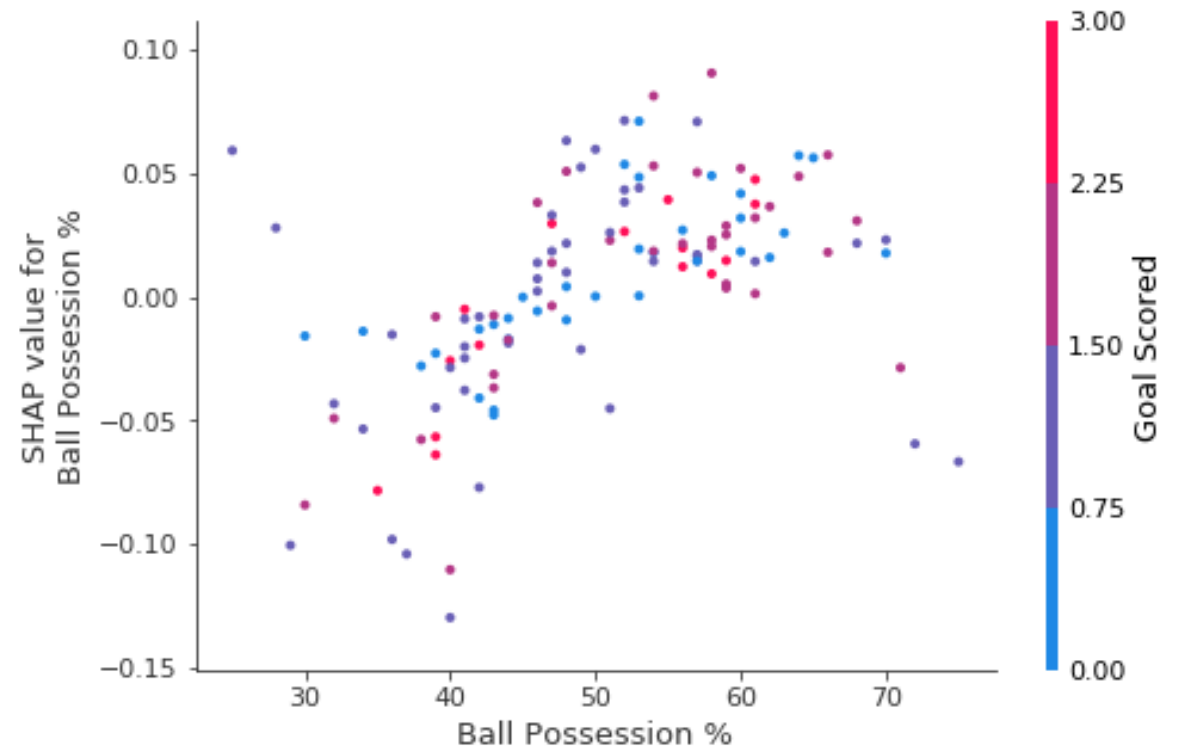


SHAP Dependence Contribution Plots



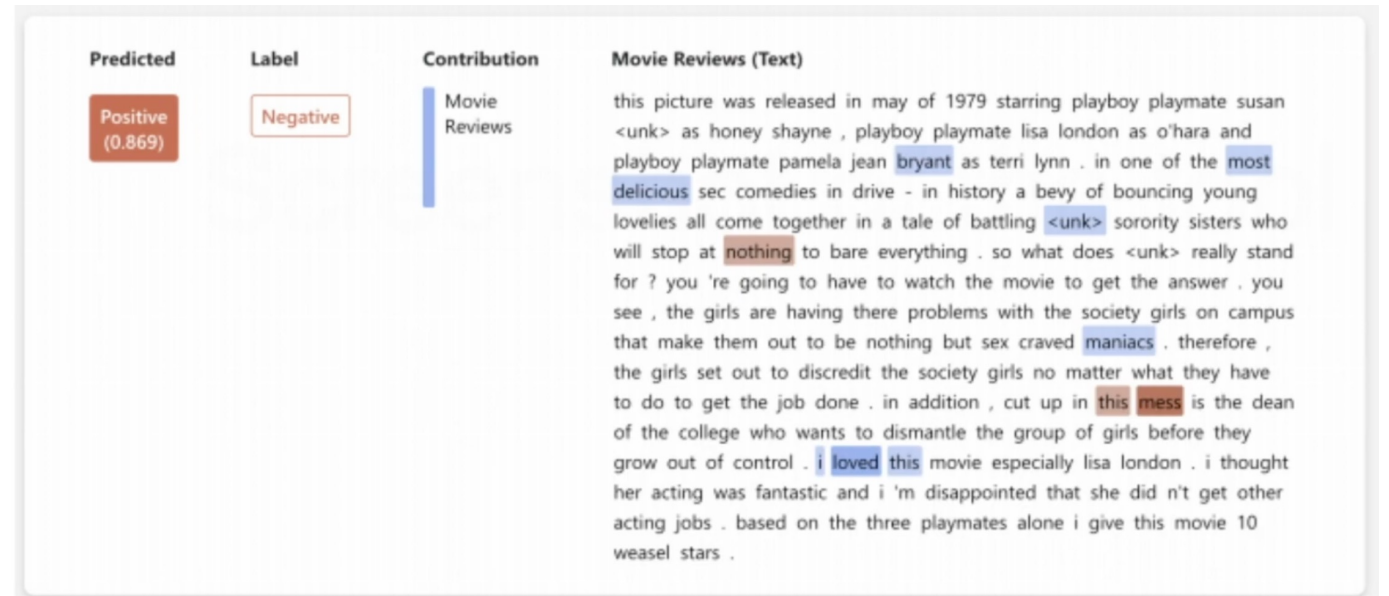
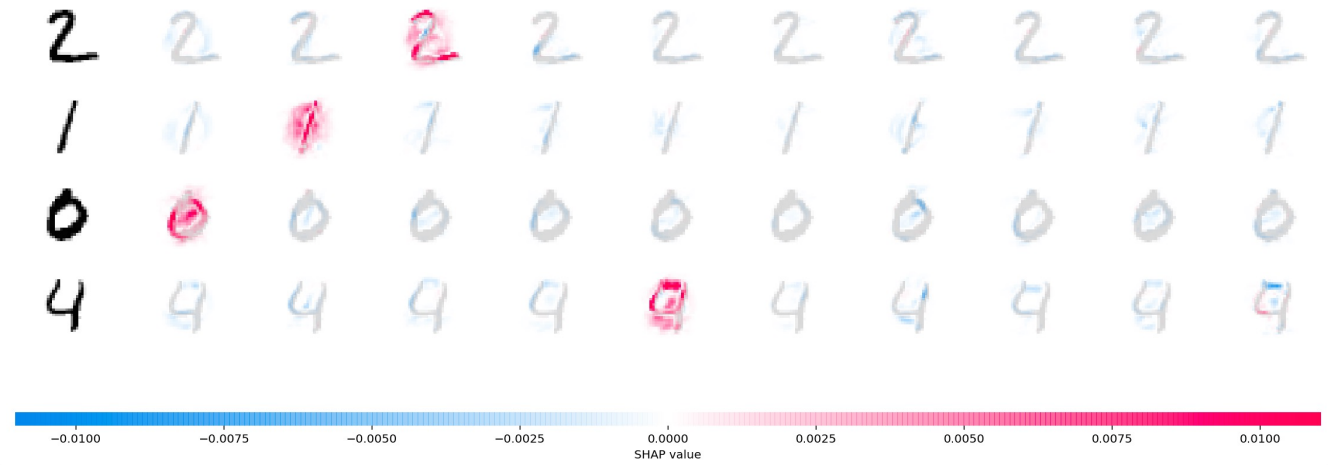
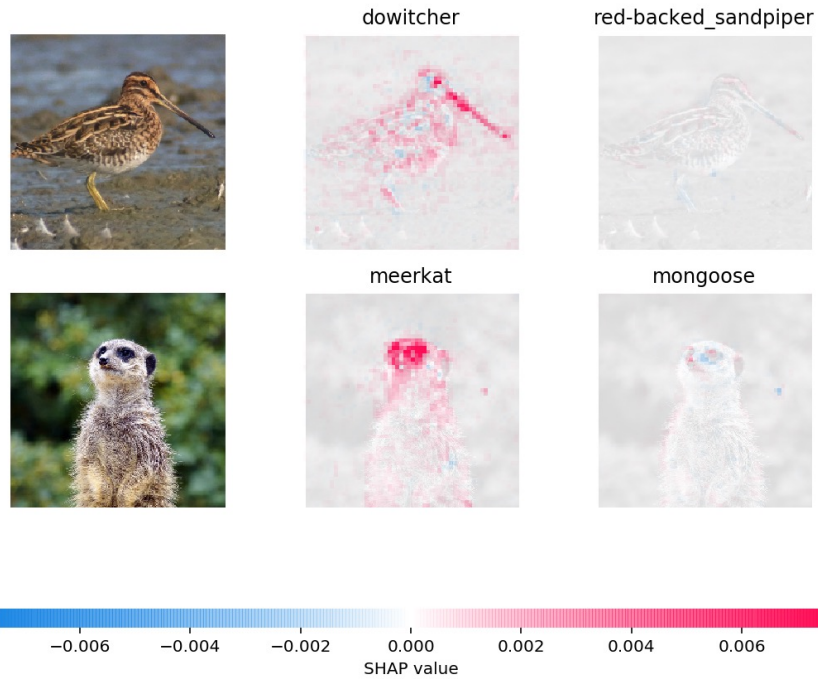
```
import shap

explainer = shap.TreeExplainer(my_model)
shap_values = explainer.shap_values(X)
shap.dependence_plot('Ball Possession %', shap_values[1], val_X,
interaction_index="Goal Scored")
```



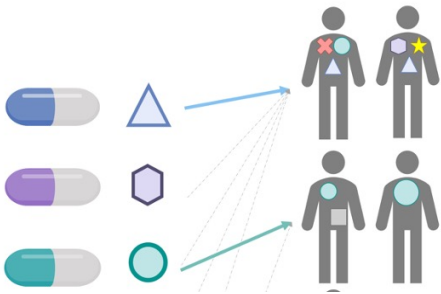
<https://github.com/shap/shap/tree/master>

Deep Learning SHAP applications



Part 2 – An application in precision medicine

Precision Medicine Challenge



Challenge

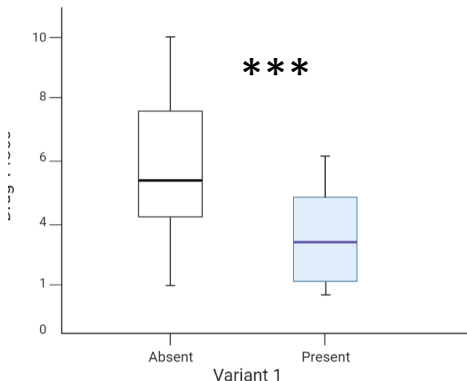
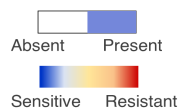
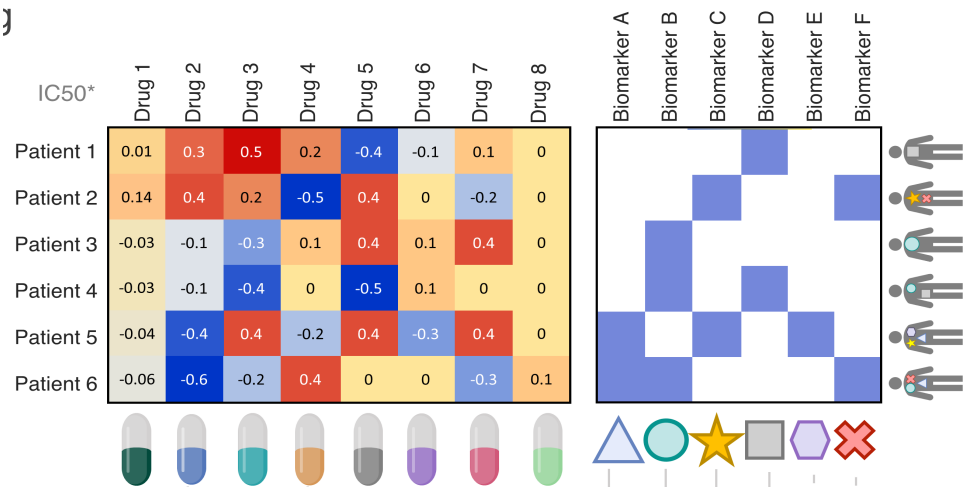
Paper 1

Paper 2

- High number of hypothesis
- Low number of observations
- Need to achieve high precision-recall
- With an explainable model - Simple to apply
- An optimization problem (minimize)



1k Samples!



$$\min_{W_{i,d}} \sum_{i=1}^S \sum_{m \in W_i} IC50_m^*$$

Number of Drugs x Number of Variants = Number of Hypotheses

200 drugs

20k variants

4M hypotheses!

Article

Identifying Lethal Dependencies with HUGE Predictive Power

Marian Gimeno ^{1,†}, Edurne San José-Enériz ^{2,3,†}, Angel Rubio ^{1,4}, Leire Garate ^{3,5}, Estibaliz Miranda ^{2,3}, Carlos Castilla ¹, Xabier Agirre ^{2,3,*}, Felipe Prosper ^{2,3,5,*} and Fernando Carazo ^{1,4,*}

- ¹ Departamento de Ingeniería Biomédica y Ciencias, TECNUN, Universidad de Navarra, 20009 San Sebastian, Spain; mgimenoc@unav.es (M.G.); arubio@tecnun.es (A.R.); ccastilla.1@tecnun.es (C.C.)
 - ² Programa Hemato-Oncología, Centro de Investigación Médica Aplicada, IDISNA, Universidad de Navarra, 31008 Pamplona, Spain; esanjose@alumni.unav.es (E.S.J.-E.); emelizalde@unav.es (E.M.)
 - ³ Centro de Investigación Biomédica en Red de Cáncer (CIBERONC), 28029 Madrid, Spain; lgarate@unav.es
 - ⁴ Instituto de Ciencia de los Datos e Inteligencia Artificial (DATAI), Universidad de Navarra, 31080 Pamplona, Spain
 - ⁵ Departamento de Hematología, Clínica Universidad de Navarra, Universidad de Navarra, 31008 Pamplona, Spain
- * Correspondence: xaguirre@unav.es (X.A.); fprosper@unav.es (EP.); fcarazo@tecnun.es (F.C.)
 † These authors contributed equally to this work.
 ‡ These authors share senior and last authorship.



OPEN ACCESS

EDITED BY
 Giuseppe Lia,
 University of Turin, Italy

REVIEWED BY
 Yu Wang,
 Shanghai Jiao Tong University, China
 Gian Maria Zaccaria,
 National Cancer Institute Foundation
 (IRCCS), Italy

*CORRESPONDENCE
 Angel Rubio
 arubio@tecnun.es
 Fernando Carazo
 fernando.carazo@veeva.com

SPECIALTY SECTION
 This article was submitted to

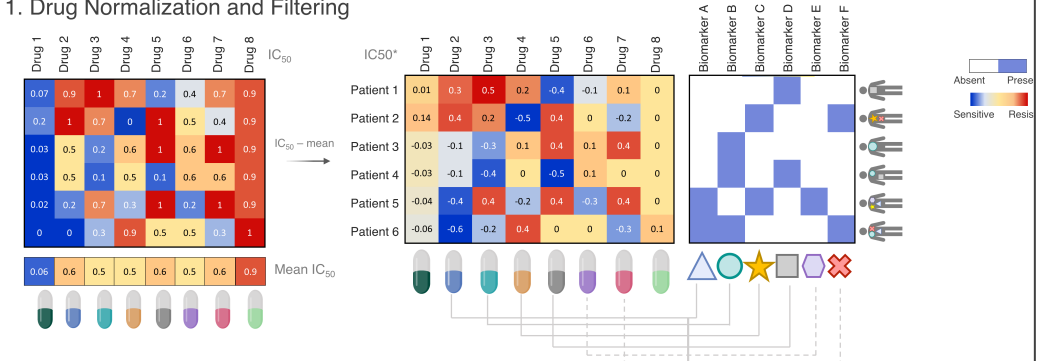
Explainable artificial intelligence for precision medicine in acute myeloid leukemia

Marian Gimeno¹, Edurne San José-Enériz^{2,3}, Sara Villar⁴, Xabier Agirre^{2,3}, Felipe Prosper^{2,3,4}, Angel Rubio^{1,5*} and Fernando Carazo^{1,5*}

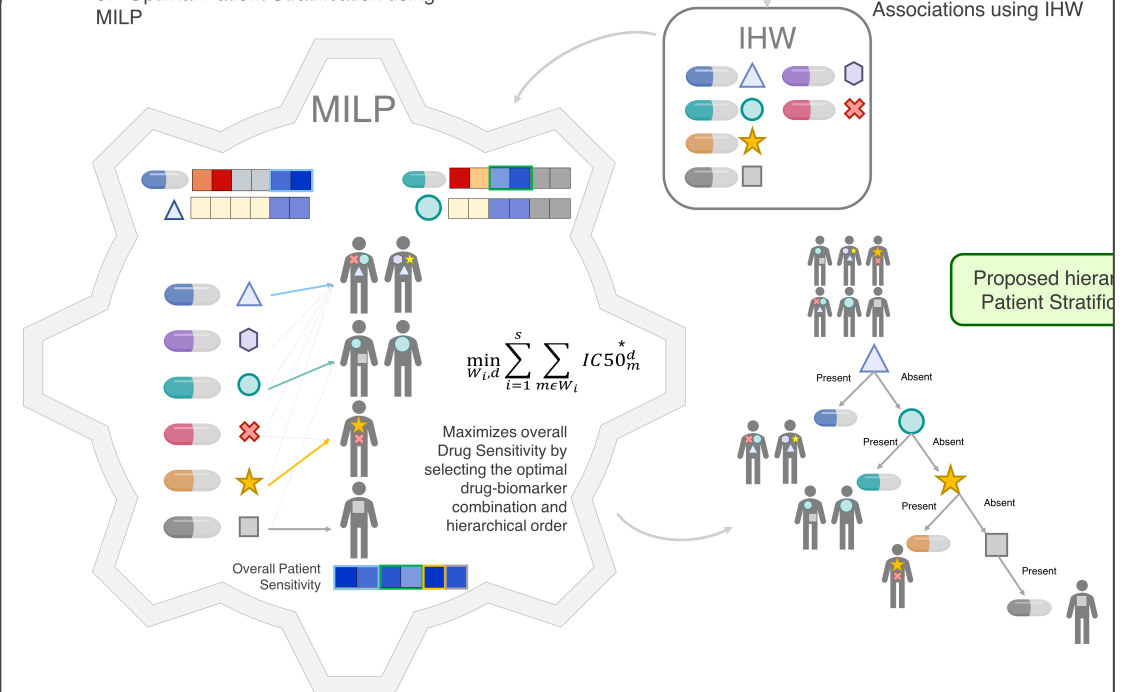
¹Departamento de Ingeniería Biomédica y Ciencias, TECNUN, Universidad de Navarra, San Sebastián, Spain, ²Programa Hemato-Oncología, Centro de Investigación Médica Aplicada, Instituto de Investigación Sanitaria de Navarra (IDISNA), Universidad de Navarra, Pamplona, Spain, ³Centro de Investigación Biomédica en Red de Cáncer (CIBERONC), Madrid, Spain, ⁴Departamento de Hematología and CCUN (Cancer Center University of Navarra), Clínica Universidad de Navarra, Universidad de Navarra, Pamplona, Spain, ⁵Instituto de Ciencia de los Datos e Inteligencia Artificial (DATAI), Universidad de Navarra, Pamplona, Spain

MOM Pipeline

1. Drug Normalization and Filtering



3. Optimal Patient Stratification using MILP



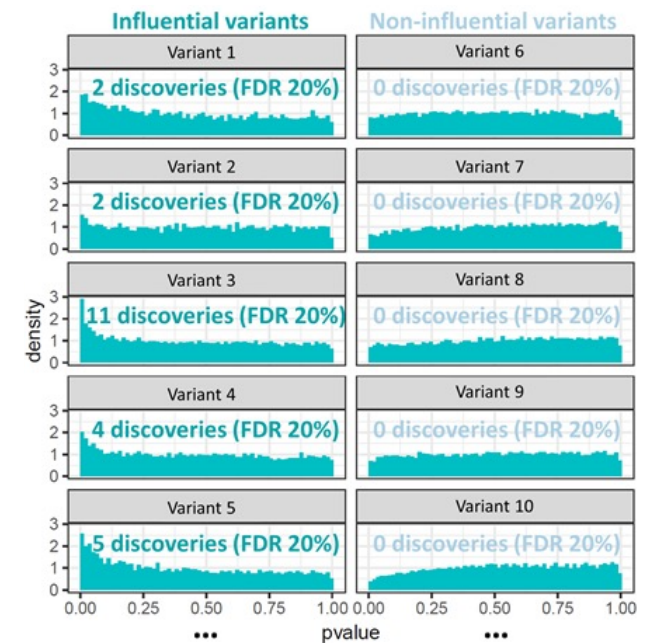
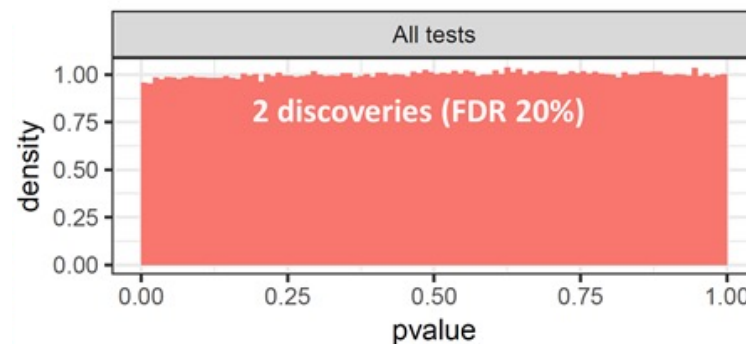
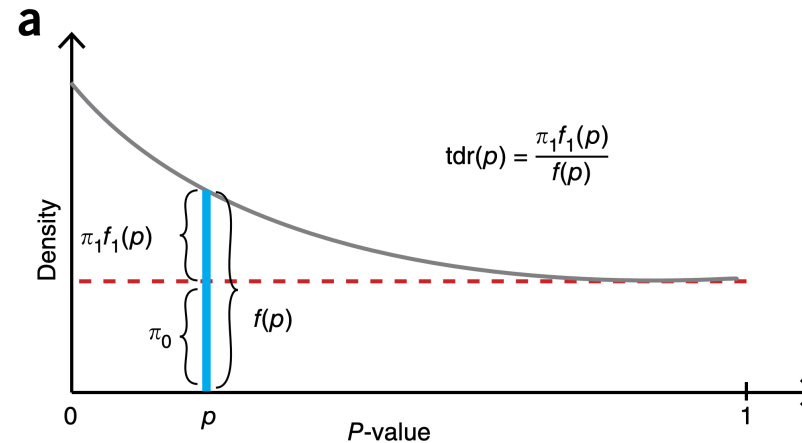
Proposed hierarchical Patient Stratification

Challenge 1. Independent hypothesis weighting

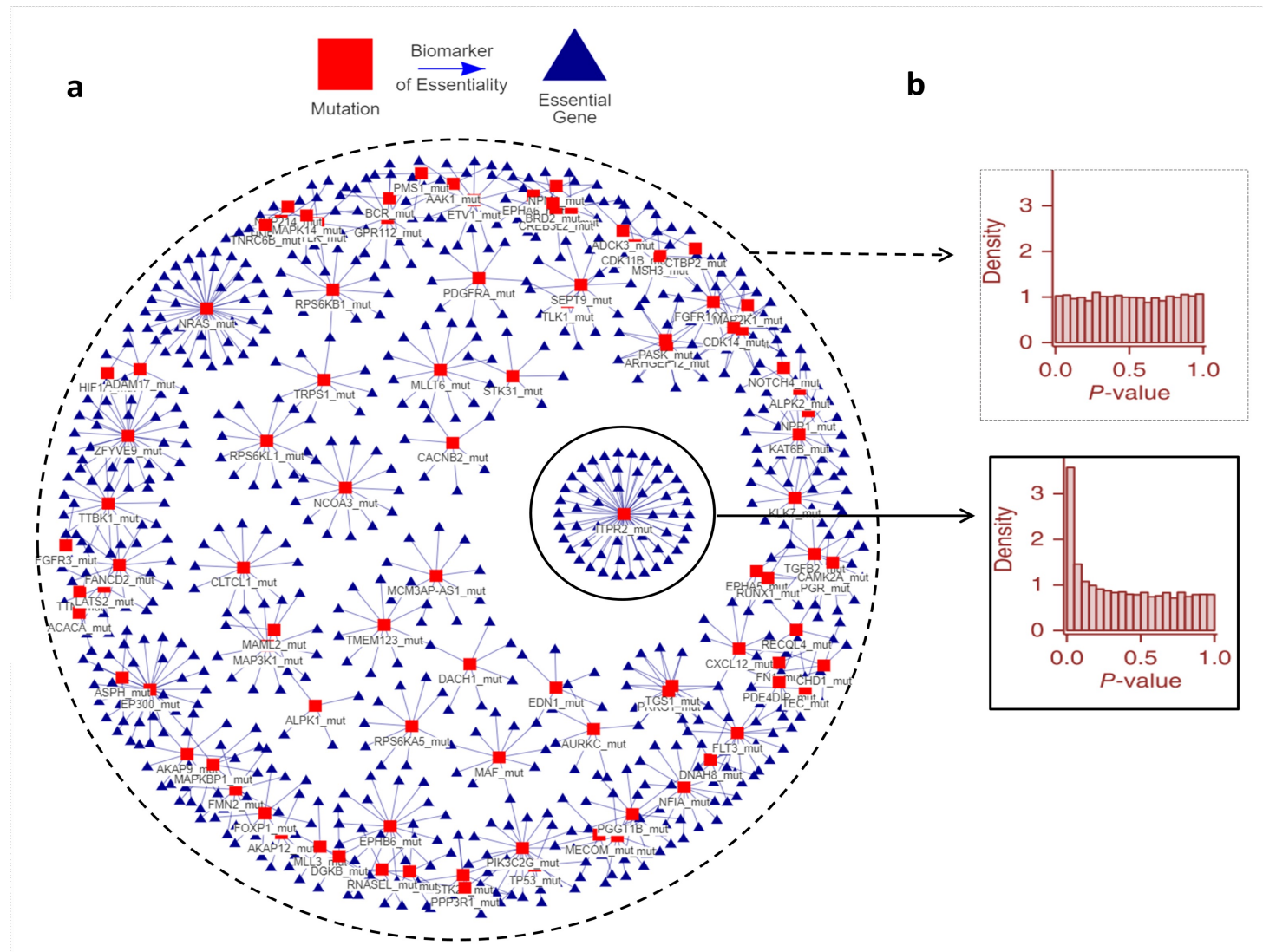
Data-driven hypothesis weighting increases detection power in genome-scale multiple testing

Nikolaos Ignatiadis, Bernd Klaus, Judith B Zaugg & Wolfgang Huber

Hypothesis weighting improves the power of large-scale multiple testing. We describe independent hypothesis weighting (IHW), a method that assigns weights using covariates independent of the P -values under the null hypothesis but informative of each test's power or prior probability of the null hypothesis (<http://www.bioconductor.org/packages/IHW>). IHW increases power while controlling the false discovery rate and is a practical approach to discovering associations in genomics, high-throughput biology and other large data sets.





Results: Hub Effect in Genetic Essentiality (HUGE)



Acute Myeloid Leukaemia HUGE effect in DEMETER

- These “hub” aberrations lead to **more statistically reliable SLs**.
- The presence of the HUGE effect means that **mutation has a different capability to define the genetic essentiality of multiple genes**.

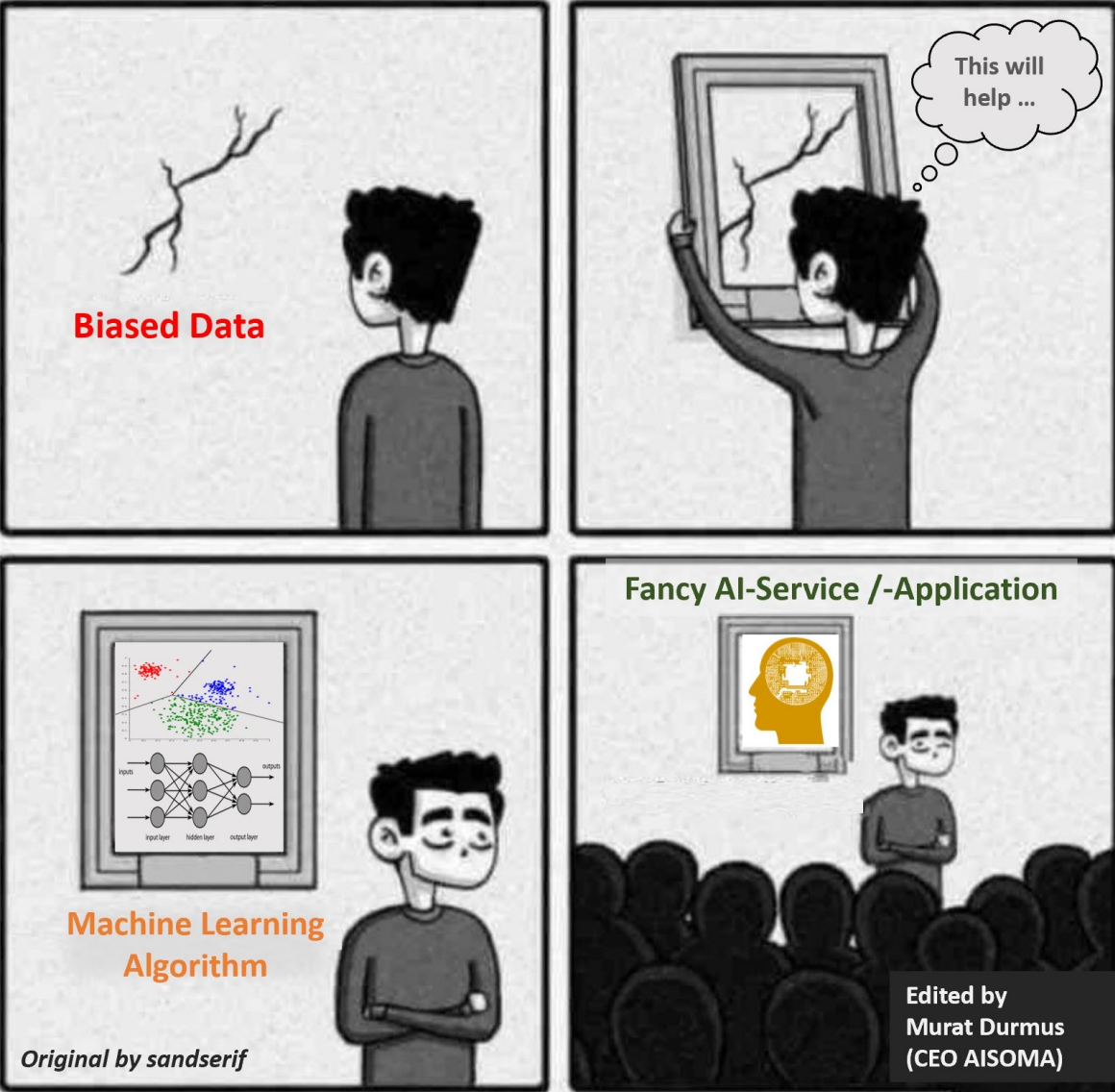
 

Article
Identifying Lethal Dependencies with HUGE Predictive Power

Marian Gimeno ^{1,†}, Edurne San José-Enériz ^{2,3,†}, Angel Rubio ^{1,4}, Leire Garate ^{3,5}, Estibaliz Miranda ^{2,3}, Carlos Castilla ^{1,†}, Xabier Agirre ^{2,3,*,†}, Felipe Prosper ^{2,3,5,*,†} and Fernando Carazo ^{1,4,*,†}

¹ Departamento de Ingeniería Biomédica y Ciencias, TECNUN, Universidad de Navarra, 2009 San Sebastián, Spain; mgimeno@unav.es (M.G.); arubio@tecnun.es (A.R.); castilla.1@tecnun.es (C.C.)
² Programa Hemato-Oncología, Centro de Investigación Médica Aplicada, IDISNA, Universidad de Navarra, 31008 Pamplona, Spain; esanjose@alumni.unav.es (E.S.J.-E.); emetizalde@unaves (E.M.)
³ Centro de Investigación Biomédica en Red de Cáncer (CIBERONC), 28029 Madrid, Spain; lgarate@unaves
⁴ Instituto de Ciencia de los Datos e Inteligencia Artificial (DATAI), Universidad de Navarra, 31080 Pamplona, Spain
⁵ Departamento de Hematología, Clínica Universidad de Navarra, Universidad de Navarra, 31008 Pamplona, Spain
* Correspondence: xaguirre@unaves (X.A.); fprosper@unav.es (FP); fcarazo@tecnun.es (FC.)
† These authors contributed equally to this work.
‡ These authors share senior and last authorship.

Thanks!



Explainable AI in Healthcare

Resources

- <https://christophm.github.io/interpretable-ml-book/>
- <https://towardsdatascience.com/using-shap-values-to-explain-how-your-machine-learning-model-works-732b3f40e137>
- <https://shap.readthedocs.io/>

