Drug repurposing for COVID-19 using explainable machine learning and mechanistic models of signal transduction circuits related to SARS-CoV-2 infection with real world data validation

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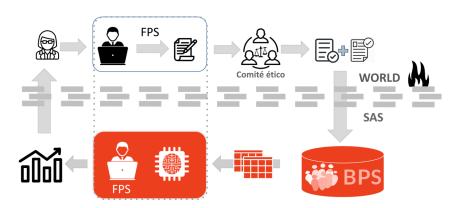






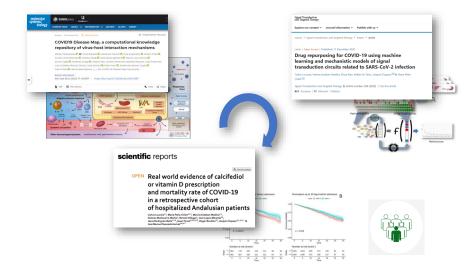


Infrastructure for secure generation of Real World Evidence from Real World Data from the Andalusian Health Population Database



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Knowledge paradigm



Knowledge discovery

Living Contradiction is a fascinating, honest examination of that genuine contradiction faced by teachers in reconciling the effort made to encourage young people towards independent critical thinking, with the simultaneous sense of responsibility to instruct and insist on a particular behavior.

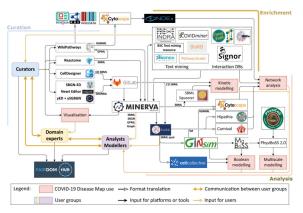
Trustworthiness

Introduction

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The WHY is as important as the WHAT

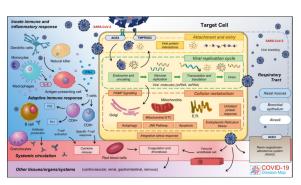
Building a COVID-19 Disease Map



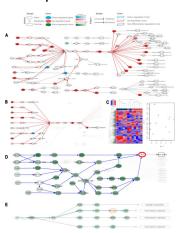
COVID-19 Disease Map¹

¹Marek Ostaszewski et al. (2021). "COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms." In: Molecular systems biology 17.10, e10387

Building a COVID-19 Disease Map



COVID-19 Disease Map¹

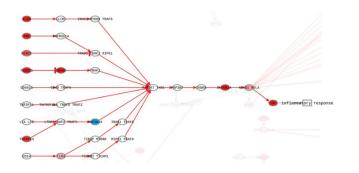


(Simplified) COVID-19 Disease Map²

¹Marek Ostaszewski et al. (2021). "COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms." In: Molecular systems biology 17.10, e10387

²Kinza Rian et al. (2021). "Mechanistic modeling of the SARS-CoV-2 disease map." In: BioData Mining 14.1, pp. 1–8

Mechanistic modeling



High throughput estimation of functional cell activities reveals disease mechanisms and p relevant clinical outcomes

PDF | HTML | Supplementary Files | How to cite | Order a Reprint Oncotarget, 2017; 8:5160-5178. https://doi.org/10.18632/oncotarget.14107

Metrics: PDF 1955 views | HTML 4565 views @

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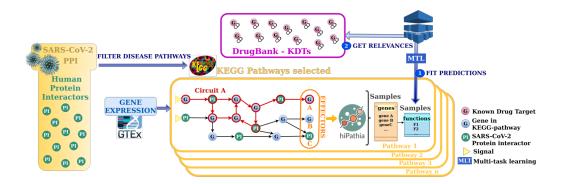
Keywords: signaling pathway, disease mechanism, prognostic, survival, biomarker

Received: September 01, 2016 Accepted: November 21, 2016 Published: December 22, 2016

$$S_n = v_n \left(1 - \prod_{s_a \in \mathcal{A}} (1 - s_a) \right) \prod_{s_i \in \mathcal{I}} (1 - s_i)$$



Drug repurposing schema



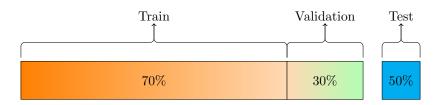
ML pipeline

Our FS model makes decissions based on the SHAP ranks We want to be true to the data

Avoid overconfidence

Introduction

- Draw from a background distribution
- Compute the explanations using a different subset

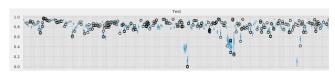


(Nogueira) Build a population (repeat the whole procedure 100 times) Make it faster: GPU-CUDA

Data-driven Validation (Performance + Explanations)

Explanation stability

Robustness Vs Stochastic, Noise, Sampling 100 Holdout splits of half the sample size Split training into learning and validation Check unbiased performance over test Compute Nogueiras¹ statistic test and CI



 \mathbb{R}^2 score distribution over the test splits

Mean R^2 : 0.82 ± 0.02 N-Stat CI: (0.729, 0.735)

¹Sarah Nogueira et al. (2017). "On the stability of feature selection algorithms." In: The Journal of Machine Learning Research 18.1, pp. 6345-6398

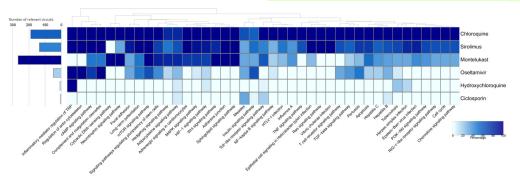
SHapley Additive exPlanations

Introduction

Fair feature responsibility attribution. Dis-aggregated by circuit by construction Additive (use biologically-relevant groups)

Template patterns

Conform a series of templates, e.g.: Affect massively almost all MAP Affect a few very specific circuits



ENDOCYTOSIS

380 KDTs (targeted by 679 drugs) have direct influence over the whole or partial parts of the map

The GO biological processes enriched are mostly related to immune activity (T-cell, inflammatory response)

The COVID-19 Hallmarks are represented

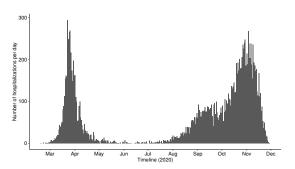
Results

DEFENSE

 Oseltamivir Basiliximab

Data facts

Andalusian public health system Year 2020, no COVID-vaccine 15968 COVID-19 hospitalized patients End point: COVID-19 certified death (28 days)



covariate	survival	death	p-value
Total N	13116	2678	
Sex (female)	6024 (45.9)	1129 (42.2)	< 0.001
Flu vaccine	5465 (41.7)	1746 (65.2)	< 0.001
Pneumococcal vaccine	3441 (26.2)	1111 (41.5)	< 0.001
Diabetes	3856 (29.4)	1167 (43.6)	< 0.001
Circulatory diseases	8111 (61.8)	2261 (84.4)	< 0.001
Cancer	1550 (11.8)	545 (20.4)	< 0.001
Respiratory diseases	2896 (22.1)	828 (30.9)	< 0.001
Dementia	964 (7.3)	536 (20.0)	< 0.001
Other mental diseases	1764 (13.4)	407 (15.2)	0.018
Anxiety and mood disorders	3382 (25.8)	784 (29.3)	< 0.001
Age			< 0.001
18_41	1399 (10.7)	20 (0.7)	
41_68	5971 (45.5)	380 (14.2)	
68_99	5746 (43.8)	2278 (85.1)	

Methods Facts

We Only include properly balanced treatments¹

964 treatments found

122 were eligible

Introduction

HR Closed-form variance estimator for Weighted Propensity Scores² Lymphocyte count registered up to 14 days since hospitalization begins Covariate-adjusted linear mixed effect model to test Lymphocyte progression trends

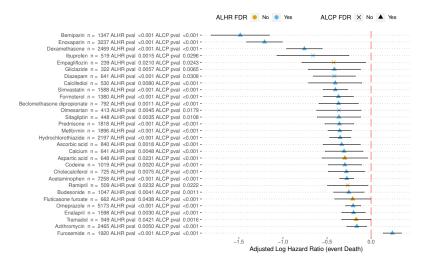
30 treatments are significant for both tests

22 after FDR adjustment

¹Elizabeth A Stuart et al. (2013), "Prognostic score-based balance measures can be a useful diagnostic for propensity score methods in comparative effectiveness research." In: Journal of clinical epidemiology 66.8, S84-S90

²David Hajage et al. (2018). "Closed-form variance estimator for weighted propensity score estimators with survival outcome." In: Biometrical Journal 60.6, pp. 1151-1163

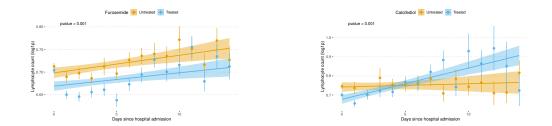
Covariate-Adjusted LHR by Treatment

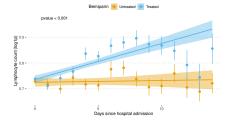






Covariate-Adjusted Lymphocyte trend





Conclusions

Bemiparin and Enoxaparin \rightarrow Highest survival

prevent thrombotic and thromboembolic complications enoxaparin has been previously reported as protective the protective effect is not shared by other anticoagulants

Calcifediol and Cholecalciferol have a protective effect

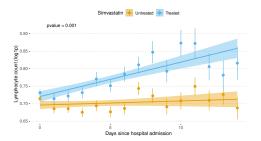
probably due to vitamin D and its pro-immune and anti-inflammatory properties2

There is a significative intersection between ML predicted drugs and RWE

$$\chi^2 = 6.674$$
, pvalue = 0.009785

Simvastatin summary





Pleiotropic effect antiinflammatory and antithrombotic inhibiting the NF-K β pathway directly reduces inflammatory cytokines (IL1, IL6, TNF- α), CRP, and neutrophils Under heavy study

Closing remarks

It is not a competition between paradigms and methods We aim to gain evidences from as many sources as possible Our \mathbf{xML} tools aim to help users **prioritize** their work:

if they *look for a needle in a haystack* help them by

(filter) removing stacks of hay prioritize what remains with biology-driven constrains and explanations

Explainability and interpretability should be **central** to ML solutions If we include explanations we need to add a **new evaluation axis**:

predictive performance is not enough

BPS, the database for secondary use of clinical data of the Andalusian Public Health System, constitutes a unique resource for large-scale RWE studies

The team

















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Thank You!