

Simulating In-Silico Clinical Research Using Diverse Real-World Data





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Introduction/Hypothesis



- Using Real-World-Data (RWD), develop in-silico models for rapidly identifying repurposed drugs that can lower the risk of death due to Sars-CoV-2 infection
- Risk of death due to COVID-19 is predominantly due to hyperactive host inflammatory responses resulting from infection

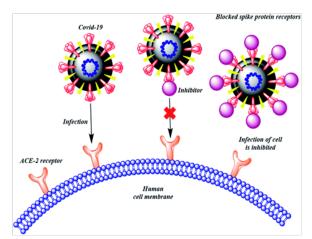
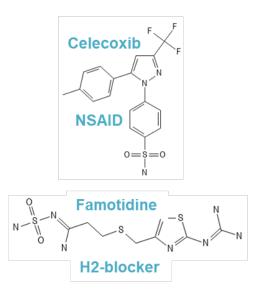


Fig 2 from https://doi.org/10.1039/D0RA04795C



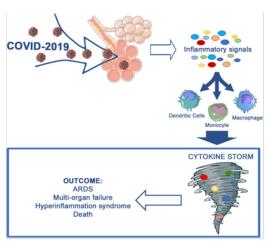


Fig1 from https://doi.org/10.3389/fimmu.2020.02132

COVID-19 Real-World-Data Sources

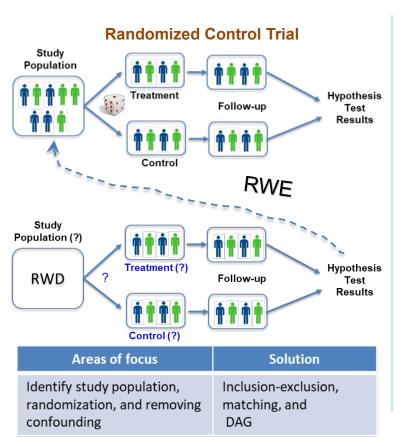


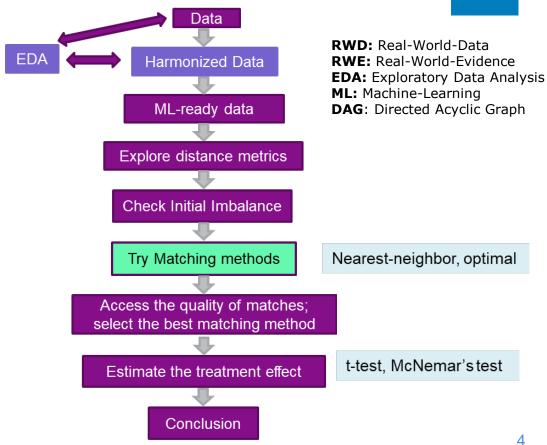
- Two appropriate RWD sources were chosen to model the causal effect of Celecoxib/Famotidine in COVID-19 patients
- Hospital data*
 - Patients (aged 18 years or older)
 - in/out-patients with documented COVID-19 diagnosis from 6/1/2020 - 1/31/2021
- Pharmacy data*
 - 120-day lookback from each patient's earliest hospital visit with a COVID-19 diagnosis

^{*} IQVIA Hospital Charge Data Master; IQVIA Longitudinal Prescription database (LRx)

Causal Treatment Effect Modeling

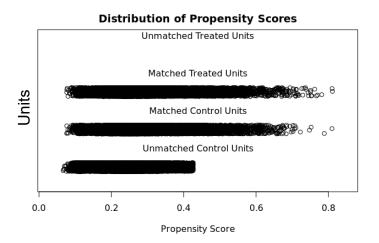




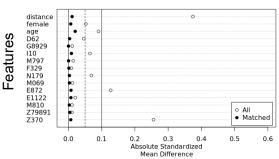


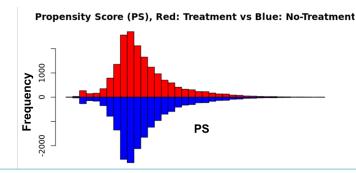
Results

Propensity Score(PS) = π_i = P(Trtmnt = 1|X_i) (for a person i)



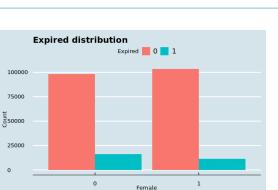
Estimating Balancing (few features are displayed)





Results shown for Famotidine; Celecoxib results are similar

$$\mathrm{SMD} = \left(\frac{\bar{x}_{treatment} - \bar{x}_{\mathrm{control}}}{\sqrt{\frac{s_{treatment}^2 + s_{control}^2}{2}}} \right)$$













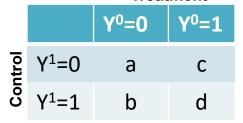


Findings

In both treatment options, among the discordant pairs, we see that there is a bigger number where the treated is the person who died, so this suggests that the treated group is at higher risk.



Treatment



 H_0 : $p_b = p_c$; H_A : $p_b \neq p_c$

p = proportion; α : 0.05; 2-sided

Exact McNemar Test

	Celecoxib				Famotidine			
Run	N	OR	CI (95%)	P-value	N	OR	CI (95%)	P-value
1	1013	2.3870	1.5498, 3.7573	3.276e-05	17916	2.400	2.2254, 2.5898	< 2.2e-16
2	999	4.5882	2.6903, 8.2730	1.642e-10	17892	2.5143	2.3304, 2.7145	< 2.2e-16
3	1019	2.0000	1.3148, 3.0927	8.200e-04	17622	2.5978	2.4045, 2.8085	< 2.2e-16
4	1026	2.3636	1.5545, 3.6669	2.326e-05	17897	2.4851	2.3029, 2.6833	< 2.2e-16
5	1046	2.4838	1.6175, 3.9002	1.115e-05	17916	2.5967	2.4056, 2.8050	< 2.2e-16

R libraries

tableone matching ipw survey tidyverse Matchit sandwich

Conclusions



- We have created a procedure to emulate an in-silico randomized control trial for estimating the causal treatment effects
- Our matched case-control study results for both Celecoxib and Famotidine show OR > 1 indicating that the exposure is associated with higher odds of death for COVID-19 patients
- This procedure can help shorten drug development, review and approval timelines, eliminate bias in data and adequate representation of trial population
- The RWE Methods pipeline can be expanded to add additional methods for new use cases like drug safety, and sequencing

OR: Odds Ratio; MSM: Marginal Structural Model; IPTW: Inverse Probability Treatment Weighting



Thank you!

Disclaimer: The information in this presentation represents the opinions of the speaker and does not necessarily represent FDA's position or policy.

