Validation of Flag, Identify, Network, Deliver: FIND FH® Using the Electronic Medical Record to Identify Familial Hypercholesterolemia within a Single Healthcare System

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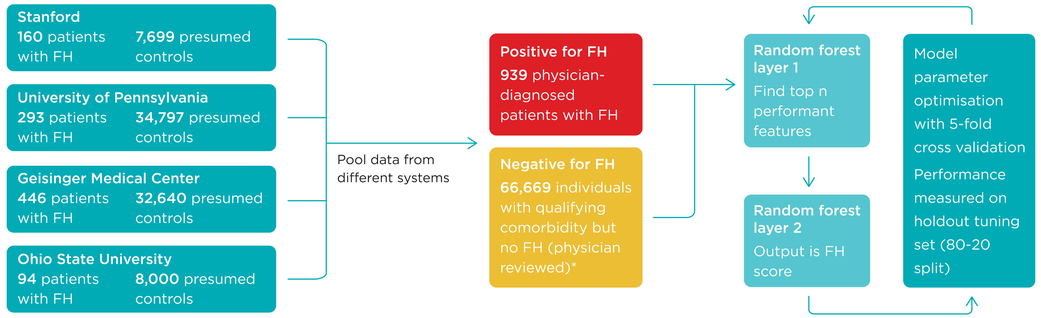
Background

Familial hypercholesterolemia (FH) is a common underdiagnosed and undertreated condition that leads to premature cardiovascular disease. A machine learning algorithm (MLA) uses artificial intelligence technology to screen for FH. We validated the use of an MLA 'FIND FH,' developed by the FH Foundation, by determining the relationship between the FIND FH score (the output of the algorithm) and either an FH clinical diagnosis or FH-causing mutation in the University of Pennsylvania Healthcare System (UPHS).

Methods and Results

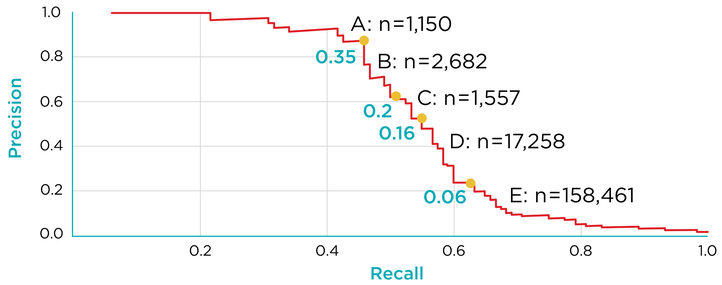
FIND FH was trained to detect FH using clinically and genetically diagnosed FH patients from four health systems.

FIND FH model training



Diagnostic performance for FH was evaluated using patients with at least one cardiovascular co-morbidity at UPHS, excluding those with a prior diagnosis of FH. Of the 700,701 individuals in the database, 181,106 had a FIND FH score above 0.0. The patients were assigned to five pre-defined strata based on FIND FH score: 'A' (>0.35), 'B' (0.20-0.35), 'C' (0.16-0.19), 'D' (0.06-0.15), and 'E' (0.0-0.05).

Total number of individuals in each of 5 study tiers from which 414 were consented



Methods and Results (continued)

While blinded to genetic results, two lipidologists reviewed medical charts on a sample of patients per strata to establish a clinical diagnosis of FH. Genetic testing was independently performed on these patients by Grifols. Chi-squared analysis and regression modeling were used to determine the relationship between FIND FH score (strata, continuous) and FH clinical or genetic diagnosis.

In the validation dataset (n=414 patients; mean [SD] age, 58.2 [14.6] years; 54% male; 79% white), the prevalence of definite or probable FH was 33% in strata A (n=109), 25% in strata B (n=109), 19% strata C (n=98), 10% in strata D (n=52), and 2% in strata E (n=46).

Summary of clinical and genetic results per FIND FH strata.

Strata	A	B	C	D	E
FIND FH score	>0.35	0.20–0.35	0.16–0.19	0.06–0.15	0.0–0.05
n=414	109	109	98	52	46
Clinical					
Definite	13	6	3	2	0
Probable	23	21	16	3	1
Possible	43	40	33	20	18
%	72%	61%	53%	48%	39%
Genetic					
No variant	90	93	84	47	38
Variant	12	10	7	1	2
% Variant	11.80%	9.70%	7.70%	2.10%	5.00%

The relationship between FIND FH score and an FH clinical diagnosis was significant per strata (p-value<0.001). The relationship between FIND FH score and FH-causing mutation was not significant per strata (p-value, 0.464) but significant with FIND FH score treated as a continuous variable (p-value, 0.013).

Conclusions

In this evaluation of electronic health record data, the MLA demonstrated a gradient between FIND FH score and likelihood of having FH. Further implementation is necessary to evaluate the applicability of FIND FH in diverse healthcare settings and the utility of the MLA to improve cardiovascular outcomes.

Disclosures

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