eMERGE	Network: External Collaborator Manuscript Concept Sheet		
Reference Number (to be assigned by CC)	NT397		
Submission Date	07/13/2020		
Project Title	Implementation of Family Health History into the health system: Recommendations for integrating MeTree platform into the EHR.		
Tentative Lead Investigator (first author)	Wiesner, Georgia		
Tentative Senior Author (last author)	Orlando, Lori		
eMERGE Site Sponsor & Contact	Sponsor: Dan Roden Contact: Sarah Bland		
All Other Authors	The study is not open to other authors. See table		
Sites Participating	Vanderbilt, Northwestern, Geisinger		
Background / Significance	Family health history (FHH) reliably identifies patients at risk for common conditions and rare genetic disorders. While several collection programs exist, FHH is not systematically integrated into health system electronic health record (EHR). MeTree is a patient facing FHH platform developed at Duke University that collects, analyzes and creates clinician decision reports on 45 inherited conditions. This is an extension grant to VUMC eMERGE site to assess the barriers and facilitators to integrating FHH into the EHR. The main outcome of this paper is to develop general guidelines for health systems to integrate FHH, such as MeTree, into their EHR. This guide will include descriptors of the major steps that each institution will need to develop in creating a health system plan.		
Outline of Project	 SA1. Create a pre-implementation assessment plan using the CFIR method for integrating the MeTree patient facing FHH collection tool into diverse EHR systems. Assessment protocols will be developed for three eMERGE sites. Domains in the CFIR pertinent to genomic medicine and FHH will be evaluation in detail across all sites. Assessment protocols will be modified for international use with the NHS-England genomics team 		

- Guided by the CFIR, conduct semi-structured interviews with key stakeholders at each site.
- Compare and contrast the implementation domains at each site, including at a minimum, EHR system requirements, workforce assessment, clinical workflow, provider value and workflow, infrastructure, institutional regulations, and data sharing and security.

<u>Deliverables:</u> The deliverable for this aim will be an implementation guide that outlines specific steps for MeTree integration into the EHR that facilitates the identification of unique institutional factors that should be considered prior to implementation. We will compare and contrast the implementation domains at each site, including at a minimum workforce assessment, clinic workflow, provider workflow, patient engagement, institutional regulations, and data sharing and security.

SA3. Demonstrate the ability to integrate FHH-driven risk assessment in EHR test systems.

- Perform a multi-domain technical assessment of the requirements for SMART-on-FHIR technology for integration of FHH into diverse EHRs in the U.S. and NHS-England.
- Demonstrate the feasibility of MeTree-EHR integration using SMART-on-FHIR by creating a test simulation environment at each eMERGE site and by deploying MeTree in at least one EHR test system.

<u>Deliverables:</u> The deliverables for this aim will be 1) an implementation guide for SMART-FHIR EHR integration for FHH risk assessment programs, and 2) demonstrate the feasibility of MeTree-EHR- SMART-on-FHIR integration by deploying MeTree in at least one EHR test system.

Desired Data - Common Variables* (Available from the CC)	□ Demographics□ ICD9/10 codes□ CPT codes□ Phecodes□ BMI	 Common Variable Labs Common Variable Meds Other: Case/Control status on Phase I and Phase II phenotypes NONE NEEDED 	
Other Desired Data (Available from participating sites)	Please specifically list out any data elements that participating sites would collect or extract from clinical or other sources for this project (i.e. not common variables above) NONE NEEDED		
Desired Genetic Data	 eMERGE I-III Merged set (HRC imputed, GWAS) eMERGE PGx/PGRNseq data set eMERGEseq data set (Phase III) eMERGE Whole Genome sequencing data set eMERGE Exome chip data set eMERGE Whole Exome sequencing data set Other (not listed above): NONE NEEDED 		
Does project pertain to an existing eMERGE Phenotype?	☐ Yes, if so please list☐ XX- No		

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Planned Statistical Analyses	Study is qualitative and descriptive in nature. Summary statistics for each paper will be presented
Ethical Considerations	Exempt- low
Available Funding or Resources	Extension grant to VUMC
Target Journal	TBD
Milestones (This section should include the key dates for completion of project, including approval, project duration, draft completion, and submission.)	Completion Summer, 2020

*Common Variables available across all datasets:

- Demographics: sex, year of birth, decade of birth, race, ethnicity
- <u>Codes</u>: (repeated values & age at event): ICD, CPT, Phecodes
- <u>BMI</u>: (repeated value & age at event) height, weight, BMI
- <u>Labs</u>: (lab name, repeated lab value & age at event) Serum total cholesterol, LDL, HDL, Triglycerides, Glucose fasting/non-fasting/unknown, & White Blood Cell count
- <u>Medications</u>: (medication name, repeated, & age at event) Cerivastatin sodium, Rosuvastatin, Simvastatin, Fluvastatin, Pravastatin, Lovastatin, Atorvastatin, & Pitavastatin
- Other: Case/Control status on Phase I and Phase II phenotype: only on GWAS dataset participants

Table of investigators and support staff for eMERGE-MeTree Project.

Not all of these individuals will be authors, as it depends on their role in each project.

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