

eMERGE Network: External Collaborator Manuscript Concept Sheet

Reference Number <i>(to be assigned by CC)</i>	NT399
Submission Date	07/13/2020
Project Title	Technical needs and processes to integrating the MeTree family health history platform into the health system EHR.
Tentative Lead Investigator <i>(first author)</i>	Lori Orlando
Tentative Senior Author <i>(last author)</i>	Wiesner, Georgia
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. This project also includes Lori Orlando, and MeTree investigators from Duke University.
Background / Significance	<p>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 reports on 45 inherited conditions.</p> <p>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 outline the technical informatic steps to integrating MeTree into the EHR of 3 eMERGE sites. Technical innovations will be described, such as the use of SMART-on-FHIR, and other APIs to the use of the platform. 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.</p>
Outline of Project	<p>The main outcome of this paper is to outline the technical informatic steps to integrating MeTree into the EHR of 3 eMERGE sites and corresponds with Specific Aim 3 of the extension grant.</p> <p>SA3. Demonstrate the ability to integrate FHH-driven risk assessment in EHR test systems.</p> <ul style="list-style-type: none"> 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.

	<ul style="list-style-type: none"> 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. <p>Deliverables: 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.</p> <p>Technical innovations will be described, such as the use of SMART-on-FHIR, and other APIs to the use of the platform. A mock integration will be performed at least 1 eMERGE site, and the barriers and facilitators will be analyzed. Strategies will be developed to overcome institutional barriers</p>
Desired Data - Common Variables* <i>(Available from the CC)</i>	<div style="display: flex; justify-content: space-between;"> <div> <input type="checkbox"/> Demographics <input type="checkbox"/> ICD9/10 codes <input type="checkbox"/> CPT codes <input type="checkbox"/> Phecodes <input type="checkbox"/> BMI </div> <div> <input type="checkbox"/> Common Variable Labs <input type="checkbox"/> Common Variable Meds <input type="checkbox"/> Other: Case/Control status on Phase I and Phase II phenotypes <input type="checkbox"/> NONE NEEDED </div> </div>
Other Desired Data <i>(Available from participating sites)</i>	<i>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)</i> NONE NEEDED
Desired Genetic Data	<input type="checkbox"/> eMERGE I-III Merged set (HRC imputed, GWAS) <input type="checkbox"/> eMERGE PGx/PGRNseq data set <input type="checkbox"/> eMERGEseq data set (Phase III) <input type="checkbox"/> eMERGE Whole Genome sequencing data set <input type="checkbox"/> eMERGE Exome chip data set <input type="checkbox"/> eMERGE Whole Exome sequencing data set <input type="checkbox"/> Other (not listed above): <input type="checkbox"/> NONE NEEDED
Does project pertain to an existing eMERGE Phenotype?	<input type="checkbox"/> Yes, if so please list <input checked="" type="checkbox"/> XX- No
Planned Statistical Analyses	Study is qualitative and descriptive in nature. Summary statistics or process analysis will be presented.
Ethical Considerations	Exempt- low risk
Available Funding or Resources	Extension funds to VUMC eMERGE parent grant
Target Journal	TBD
Milestones <i>(This section should include the key dates for completion of</i>	Completion Summer, 2020

***Common Variables available across all datasets:**

- Demographics: sex, year of birth, decade of birth, race, ethnicity
- Codes: (repeated values & age at event): ICD, CPT, Phecodes
- BMI: (repeated value & age at event) height, weight, BMI
- Labs: (lab name, repeated lab value & age at event) Serum total cholesterol, LDL, HDL, Triglycerides, Glucose fasting/non-fasting/unknown, & White Blood Cell count
- Medications: (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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