

Advancing Precision Healthcare for Veterans through HPC systems, & large-scale Artificial Intelligence/Machine Learning

> **Request for Concept Ideas Information Webinar**

> > November 18, 2021

VA, Million Veteran Program (MVP) & Department of Energy (DOE)



Agenda

- 1. Overview (Sumitra Muralidhar, PhD Director, MVP & VA-DOE Joint Research Program)
 - Scope & Timeline
- 2. Data Availability & Computing Environment
 - VA & MVP Cohort (Kelly Cho, PhD & Lauren Costa, MPH MVP Data Core)
 - Computing Environment Description (Brett Ellis ORNL, DOE)
- 3. Examples from Current Projects
 - MVP gwPheWAS (Ravi Madduri, PhD ANL, DOE)
 - Suicide Prevention Exemplar (Ben Mcmahon, PhD LANL, DOE)
- 4. Q&A (30 mins)

Request for Concepts - Overview

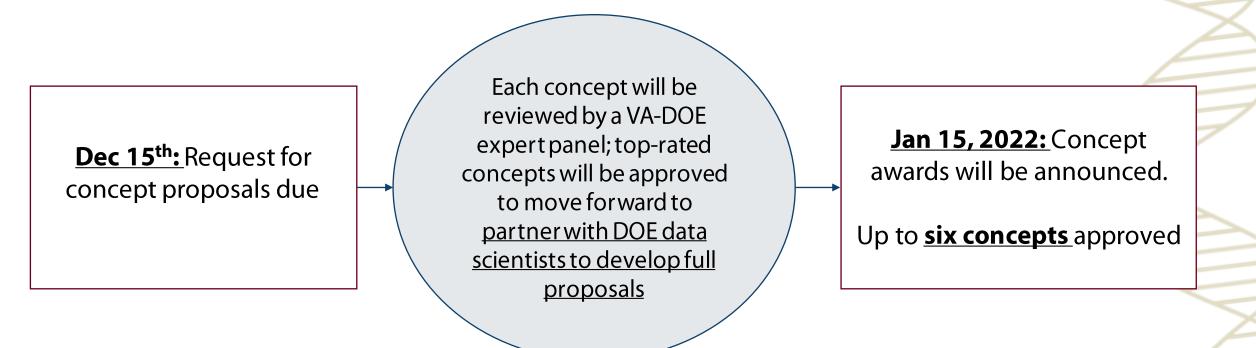
Purpose: Address clinical care gaps where high-performance computing (HPC), artificial intelligence (AI), and machine learning (ML), can be used to improve medical knowledge and be applied to improve healthcare delivery in the VA

Focus: The primary goal of these clinical concept ideas is to create new tools and technologies for predicting disease risks and outcomes by applying advanced computing and Al/ML to VA clinical data and where applicable, MVP genetic data.

Eligibility

- Applicant must be 5/8ths VA
- Should demonstrate a requirement for HPC computing resources at DOE (ORNL)

Requests for Concepts - Timeline



Submit questions and concept proposals to MVPLOI@va.gov

Full proposals will be funded for 2 years For VA investigators- up to \$250,000/year DOE scientists-TBD

Application Instructions

- Provide a summary of the concept idea addressing the topics below (5 pages maximum) using the template provided
 - Abstract- summary of the concept idea
 - Specific Aims concisely state the gap in clinical care and the potential gain by employing HPC and AI/ML tools and the specific aim(s) to be achieved
 - Research Strategy background, significance, innovation
 - Study population and data source (s) description of data needed
 - Impact and implications of the proposed concept idea including relevance to Veterans/VHA health care)
 - Literature Cited
 - Key personnel involved and bio sketches



Available Data & Computing Environment

Kelly Cho & Lauren Costa - MVP Data Core Brett Ellis – R+D Group Leader (ORNL, DOE) Jeremy Cohen – ORNL Lead, MVP CHAMPION

Data Availability in KDI (Knowledge Discovery Infrastructure) ORNL, DOE

VA Cohort (~24 Million)

 $CDW \ ({\sf Corporate \, Data \, Warehouse}) \ Production - Updated \\ Nightly$

TIU Notes (Text Integration Utilities) including radiology – update nightly

Raw Domains*: Oncology, others per request

OMOP (Observational Medical Outcomes Partnership, Common Data Model)

CART (clinical assessment reporting and tracking)

CAN Score (Clinical assessment of nutrition)

Others by Request*

*Note: transfer is manual and may take time to move over

Notes:

- Additional data sources may be available upon request (such as National Death Index, Pathology domain, geographic location)
- Centers for Medicare and Medicaid Data **not currently available** in KDI Servers in ORNL, DOE request in progress
- VitalStatus data **not currently available** in KDI servers request in progress

MVP Research-Ready Data

MVP Baseline Survey & MVP Lifestyle Survey



MVP is a Research Data Repository
 MVP Data Core and MVP Genomics Core manage and prepare the clinical and genetic data to provide to MVP Researchers/Projects in coded data fashion in all MVP

- ☐ Current MVP cohort available for research
 - ☐ Enrollees Roster **V20.1** (**N=819,417**)
- MVP Surveys

environments

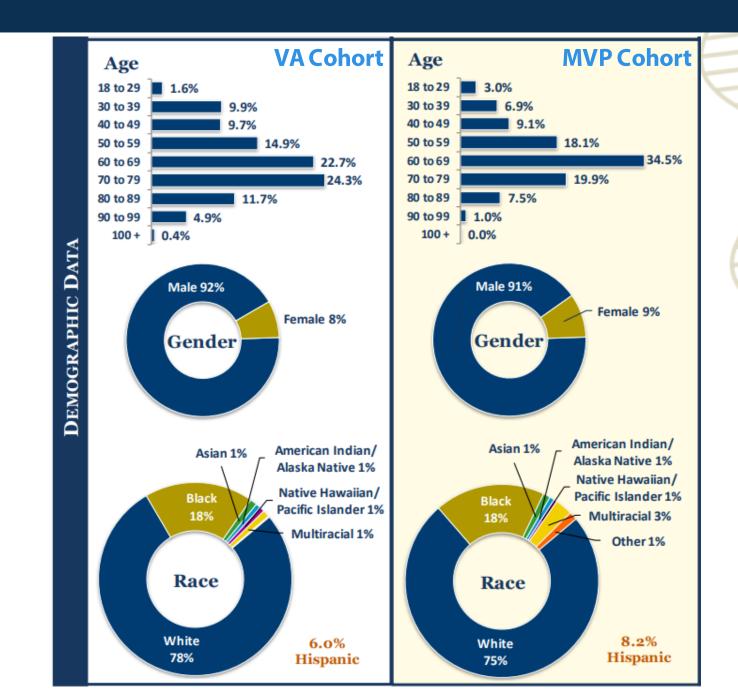
- > ~60% Completed Baseline Survey
- > ~45% Completed Lifestyle Survey
- MVP Genomics Data
 - Genotype Release V4.0 (N= 658,311)
 - ➤ 1000G+African Genome Resources imputation of release V4.0 genotypes
- ☐ Clinical EHR data from CDW
- ☐ Other Data Sources

Cohort Demographics

Age

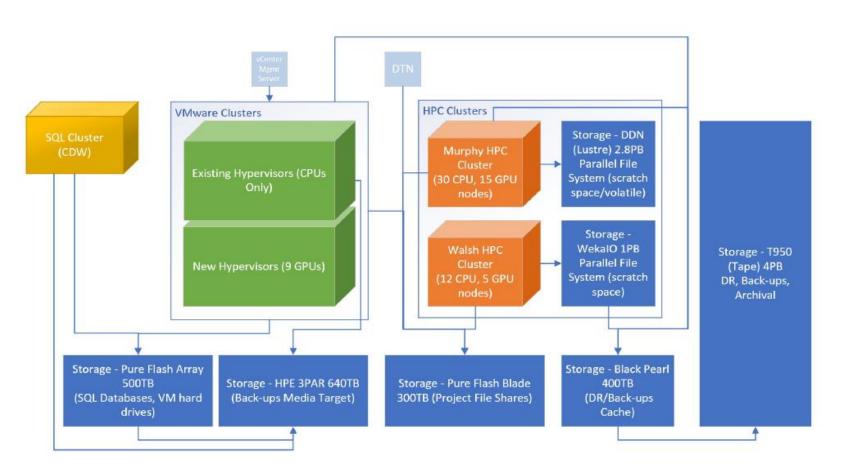
Gender

Race



MVP- CHAMPION System Capabilities

KDI Enclave Topology v.1.2 – KDI.VA.Champion Systems Quick Reference 11/09/2021







CHAMPION Architecture – Murphy vs. Walsh Storage

"Loretta Walsh of the U.S. Navy. Loretta was the first woman to enlist in the Navy and also the first woman allowed to serve in any of the U.S. Armed Forces as anything other than as a nurse. Walsh subsequently became the first woman U.S. Navy petty officer when she was sworn in as Chief Yeoman in 1917. We honor her service. Fair winds and following seas."

Dept of Veterans Affairs. May 17,2015 (Facebook)

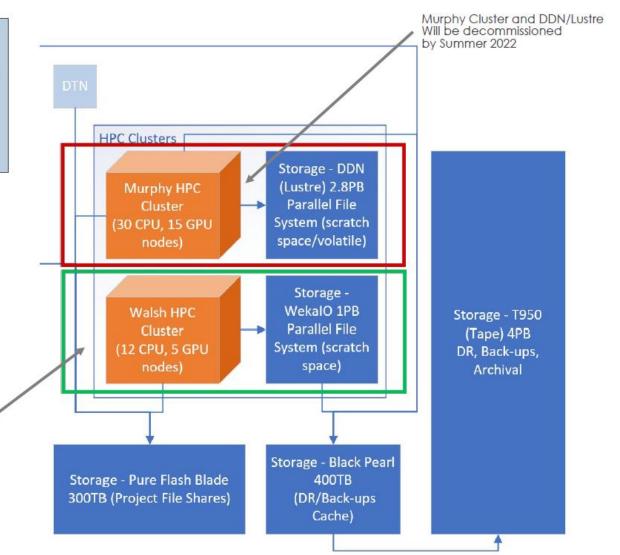
http://navylog.navymemorial.org/walsh-loretta

Resource Utilization Committee (RUC):

- Access
- Dedicated run time

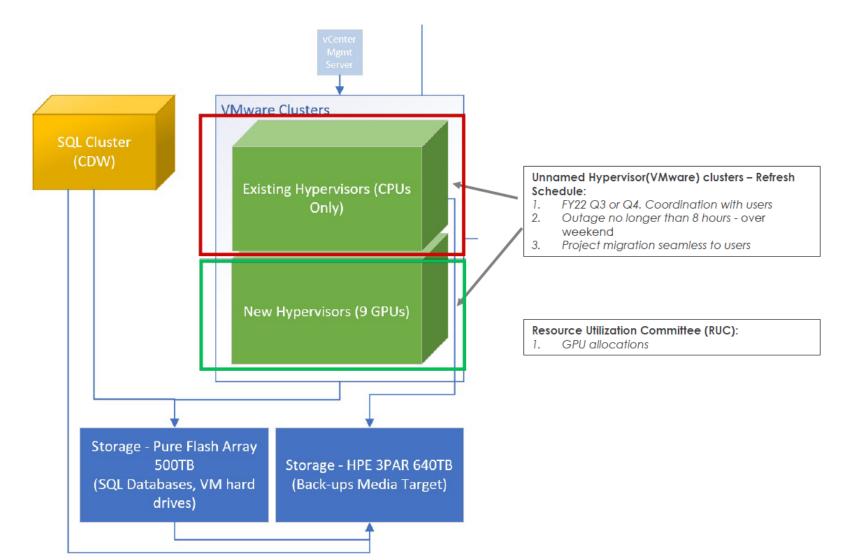
Walsh Build - Schedule:

- November & December 2021 Build and initial test
- January & February 2022 Test with core team and selected group of MVP users
- March 2022 All users migrated
- 4. April & June 2022 Work closely with users
- 5. June 2022 Murphy decommissioned





MVP-CHAMPION Architecture – Hypervisors (VMs) & SQL cluster, Storage



*****OAK RIDGE

Hypervisors (VMs): GPU Performance and Memory

GPU Specifications (not available for current hypervisors)

| | Existing | New |
|--------------|----------|-----------|
| Manufacturer | - | NVIDIA |
| Architecture | - | A100 40GB |
| Release Date | - | 2020 |
| Count | - | 6 |

GPU Performance (not available for current hypervisors)

| | Existing | New |
|------------------|----------|------------|
| GPU Performance | - | A100 40GB |
| Double-Precision | - | 9.7 TF |
| Single-Precision | - | 19.5 TF |
| Memory Bandwidth | - | 1,555 GB/s |

No GPUs were provisioned as a part of the original hypervisor cluster. Using information from user feedback it was determined that providing virtual GPUs (vGPUs) in the new cluster would enable development of AI/ML code that could leverage the capability and be ported to HPC systems.

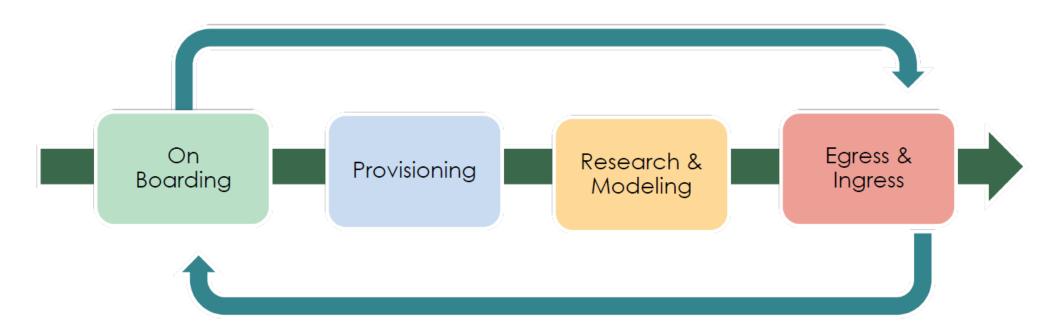
Hypervisor Memory

| | Existing | New |
|-----------------|----------|------|
| Memory per Node | 512GB | 2TB |
| Node Count | 11 | 6 |
| Total Memory | 5.5TB | 12TB |

The available memory in the cluster has been doubled. Using information from user feedback and analysis of

Project Lifecycle

Project Lifecycle will continue following established processes





KDI/ORNL Services and Support

- Security & Management Services
 - Monitoring & remediation of malware and vulnerabilities
 - Software Catalog including several scientific computing repositories (CRAN, Bioconductor, PyPi, Anaconda, etc.)
 - Account management
 - Log aggregation to Security Information and Event Management (SIEM)
 - Patch management
- Support Services
 - User on-boarding and training
 - Tier 1 user support: login/account assistance, software installations, ingress/egress request processing, general troubleshooting
 - Tier 2 support: advanced troubleshooting, custom system implementation
 - Tier 3 support: advanced system engineering, coordination with vendor support teams
 - Database Administration: query performance tuning, database management



Using Summit Supercomputer for analysis that needs extreme scale

Joint work with Oakridge Leadership Computing Facility (OLCF)

Ravi Madduri

Oakridge Leadership Computing Facility - Summit

- Named fastest super-computer in 2018 with 148.8 PF and now ranks second in the world
- GPUs on Summit are ideal for scaling up analysis and do largescale deep learning experiments
- We are using the GPUs on Summit to conduct a genome-wide Phenome wide association study in MVP to generate a summary data resource for the research community
- Data management pipelines to and from Summit exist
- Mechanisms exist to request compute time on Summit



Specifications and Features

Processor:IBM POWER9TM (2/node) **GPUs:** 27,648 NVIDIA Volta V100s (6/node)

Nodes:4,608

Node Performance: 42TF

Memory/node: 512GB DDR4 + 96GB HBM2

NV Memory/node: 1600GB

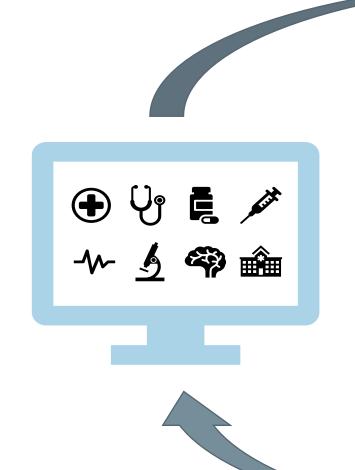
Total System Memory: >10PB DDR4+ HBM + Non-volatile **Interconnect Topology:** Mellanox EDR 100G InfiniBand,

Non-blocking Fat Tree

Peak Power Consumption: 13MW

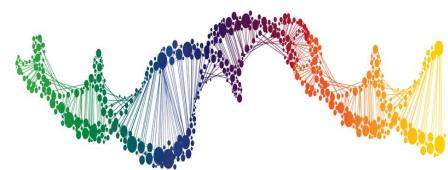
Genome-wide PheWAS (Core Analysis)

An example of extreme-scale compute on Summit



GWAS looks for associations with a specific phenotype across the entire genome

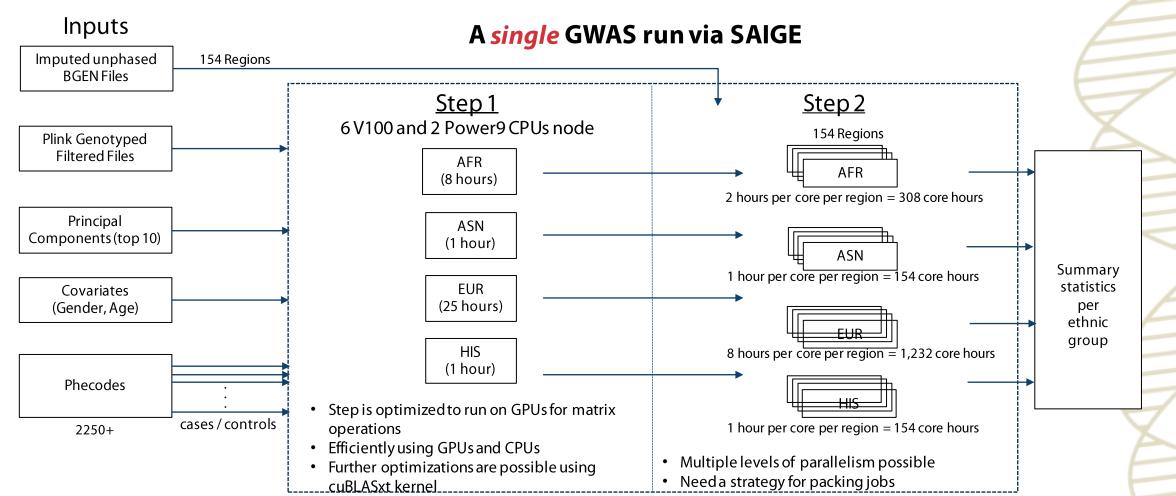




PheWAS looks for associations with a specific genotype across the entire phenome

Analysis plan on Summit

• Over 2250 phenotypes and each needs to be run individually through SAIGE which amounts to 9000 GWAS runs.





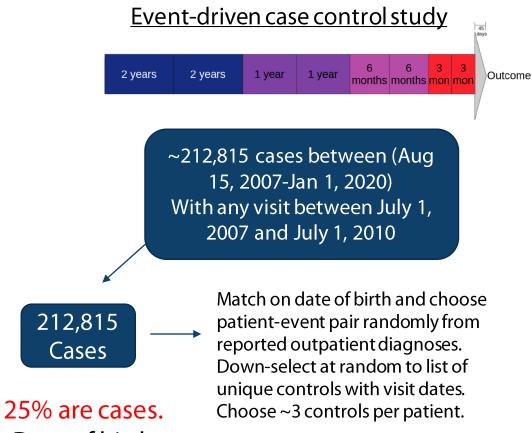
Predictive modeling with the DOE

Ben Mcmahon

Predictive modeling with the DOE

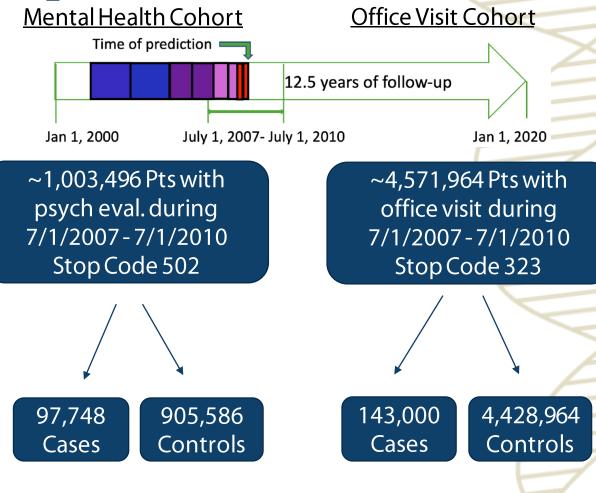
- DOE has defined workflows that
 - Extract and staging most types of structured data,
 - Create several appropriate study designs
 - Train a variety of predictive models (Logistic regression, Cox, ML/AI)
 - Transfer models across study designs
 - Evaluate and visualize model performance in defined subgroups
- DOE has also explored incorporation of genetics and natural language processing (NLP) information into models.
- DOE has teams with expertise in longitudinal modeling, transfer learning, multimodal data analysis, NLP, and genetics

Example cohort construction, for Suicide, Suicide Attempt, and Overdose



Date of birth matched. Sampled such that density of visits is similar.



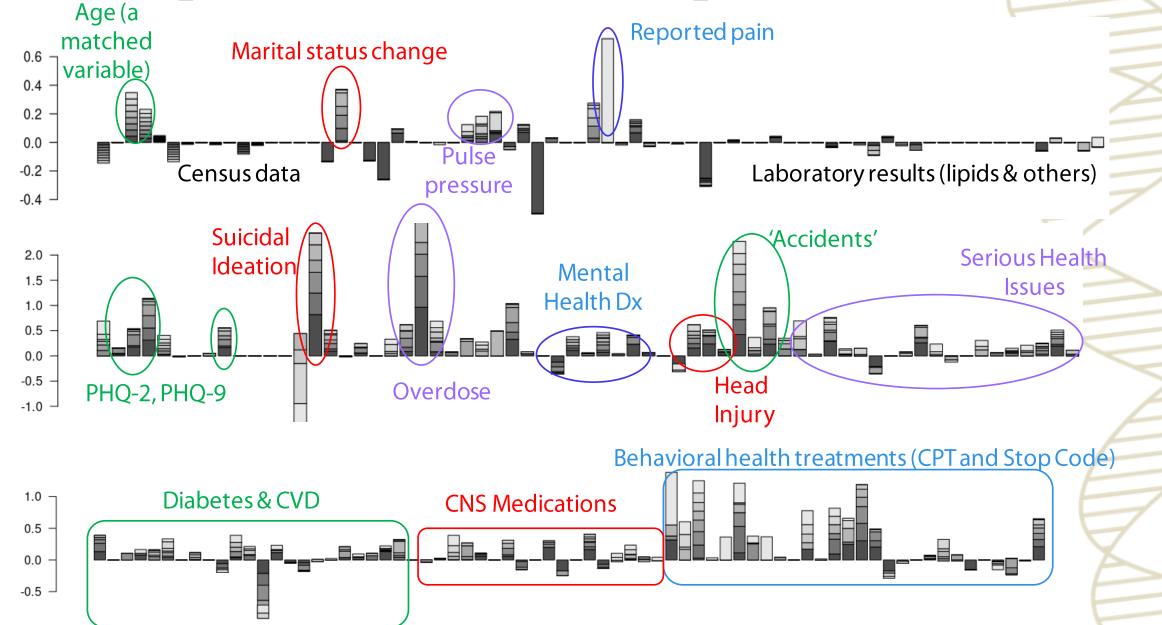


Prediction is made 2 weeks after psych eval. or office visit.

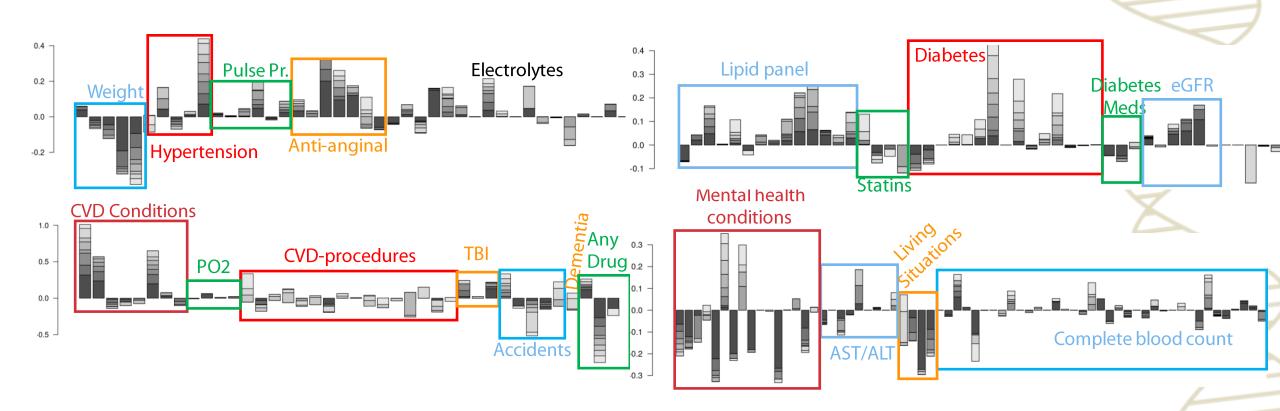
9.7% are cases

3.2% are cases

Example results for suicide prevention study



Example results for CVD study



For both suicide prevention and cardiovascular disease, we are able to train time dependent predictive models across a broad range of data types, including diagnosis, medication, procedure, survey, demographics, and laboratory data.

These codes are extensible to other problems

Workflow for predictive modeling

- Staging of structured data
 - Two-stage data staging, across roles (MVP, CDW, notes) and projects
 - Patient clustering with SOMs and trajectories towards mortality
- Development of predictive models (acute suicide risk)
 - Baseline linear hazard models with variable selection
 - Multi-modal predictors with error tolerance
 - Longitudinal trajectories
 - Combinatorial predictors
 - Incorporation of novel data types (NLP, genetics)
- Natural language processing
 - Improved sensitivity for targeted variables (eg. homelessness)
 - Providing additional information on patient visits (ctakes)
 - Identify novel predictive concepts through advanced NLP
- Genetics
 - Staging and Q/C of data; accumulation of best-practices for SNP arrays
 - Creation of polygenic risk scores and identification of mechanistic correlations
 - Processing and staging of genome sequence data
- Decision support
 - Engage clinicians and REACH-VET: What do you need?
 - Subgroup analysis in terms of existing frameworks (epi, SOC, mechanistic)

We look forward to collaboration across the VA research community to improve Veteran care!

Please contact MVPLOI@va.gov with any questions

Use subject header "VA DOE RFA"

Q+A