

Introduction to the VA PHENOMICS LIBRARY (VAPheLib)

Sponsored by the Million Veteran Program (MVP)
on behalf of the Office of Research and Development

VA Webinar - May 12, 2020

Kelly Cho, PhD, MPH

Million Veteran Program (MVP) &
Cooperative Studies Program Epidemiology Center (CSPEC) and Data Science
VA Boston, MA

VA



U.S. Department
of Veterans Affairs

DISCOVERY ★ INNOVATION ★ ADVANCEMENT

VAPheLib Introduction

Purpose:

The purpose of this seminar is to provide an introduction to a new Office of Research Development initiative to develop a centralized VA Phenomics Library.

Learning Objectives:

1. Participants will learn about the goals and structure of the VAPheLib.
2. Participants will learn how to best navigate and use VAPheLib.
3. Participants will learn how to contribute and build a partnership with current expansion of VAPheLib to the national VA-wide community.

Outline

- Background
- EHR Phenotyping
- VAPheLib Project Plan
- Current State
- VAPheLib Demonstration
- Feedback and Next Steps
- Questions



VA's *Phenomenal Phenomics* Library Team

❖ Sponsored by VA ORD under Dr. Rachel Ramoni in collaboration with MVP, CSP and VINCI

Key Partners and Contributors

THANK YOU!

- **MVP** (Million Veteran Program - Director: Dr. Sumitra Muralidhar)
 - Co-PIs: Dr. Mike Gaziano, Dr. Chris O'Donnell, Dr. Phil Tsao/Executive Director: Dr. JP Casas
 - Full MVP Consortium Acknowledgement:
 - https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/MVP_Consortium_Acknowledgement
 - MVP Project Investigators (35 Projects and 400+ study team members)*
- **CSP** (Cooperative Studies Program - Director: Dr. Grant Huang)
 - **CSPEAR** (CSP Epidemiology Analytics Resource)
 - Mihaela Aslan, PhD, Michael Gaziano, MD, MPH, Dawn T. Provenzale, MD, MS, Nicholas L. Smith, PhD, Philip Tsao, PhD
 - **Boston CSP Epi Center** (Director: Dr. Michael Gaziano)
 - David Gagnon, Katherine Kurgansky, Brian Charest, Jin Park, Melissa Young, Joy Vetter, Daniel Posner
- **VINCI** (VA Informatics and Computing Infrastructure - Director: Dr. Scott DuVall)
 - Jeff Scehnet, Kevin Malohi, Tori Anglin, and many others
 - **COVID19 Shared Data Resources Team** (Presented by Dr. Scott DuVall on April 22, 2020)
- **VACS** (Veterans Aging Cohort Study - PI: Dr. Amy Justice)
 - Chris Rentch, Melissa Skanderson, Janet Tate, George Hauser, Farah Kidwai-Khan, Lesley Park

✓ more information about our
Partners and Contributors:
https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Contributors_and_Partners

VA's *Phenomenal Phenomics* Library Team

- **MVP Project Investigators (35 Projects & 400+ study team members)**

CSP575B/MVP025: Joel Gelernter, Murray Stein

MVP001: Peter Wilson, Kelly Cho

MVP003/MVP028: Phillip Tsao, Kyong-Mi

MVP005/MVP024: Neal Peachy

MVP007: Marcas Bamman

MVP009: Lawrence Phillips

MVP011: Jean Beckham, Nathan Kimbrel, Phillip Harvey, David Oslin, Benjamin McMahon

MVP012: Kyle Kampman

MVP014: Scott Damrauer, Christopher O'Donnell, Phillip Tsao, Ravi Madduri

MVP015: Mark Logue

MVP017: Amy Justice, Michael Gaziano, Francis Alexander

MVP018: Jennifer Lee

MVP020: Donna White

MVP022: Richard Hauger

MVP026: Victoria Merritt

MVP030: Jason Vassy

MVP032: Reid Thompson

MVP034: Shaija Shah

BDS002: Saiju Pyarajan

MVP002/MVP027: Adriana Hung

MVP004: Amy Justice, Henry Kranzler

MVP006: Panagiotis Roussos

MVP008: Shiu-Wen, Cynthia Brandt, Sally Haskell

MVP010: Alan Ryan

MVP013: Steven Zelidat

MVP016: Jennifer Lee, Tim Assimes

MVP019: James Ashe

MVP021: Edward Siew, Michael Matheny

MVP023: Fatemeh Hahgighi

MVP029: Dawn Provenzale, Drew Helmer

MVP031: Bruce Montgomery

MVP033: Marianna Gasperi

BDS001: Nikhil Munshi, Saiju Pyarajan

THANK YOU!

- ✓ **Plus many others...**
- ✓ **Growing list of contributors!**

https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Contributors_and_Partners

- **MVP-VAPheLib is managed and maintained by MVP Data Core: MVPDataCore@va.gov**

(Lauren Costa, Anne Ho, Petra Schubert, Laura Tarko, Nicholas Link, Katherine Liao, Tianxi Cai, Mai Nguyen, Rebecca Song, Hanna Gerlovin)

VA's *Phenomenal Phenomics* Library Team

VAPheLib Program Team – Key Personnel:

- **VACO Lead:** Sumitra Muralidhar, Ph.D
- **Director:** Kelly Cho, Ph.D, MPH
- **Project Management:** Ashley Galloway, MPH
- **Coordinator:** Regina Joseph, MPH
- **Systems Support Librarian:** Jeff Gosian, BS
- **Data Operations Lead:** Anne Ho, MPH
- **Data Services Specialist:** Rahul Sangar, MPH
- **Computer Programmer:** Michael Murray, MPH
- **Computing Environment and System Administration:** VINCI (Scott DuVall, Ph.D, Kevin Malohi, BS and Tori Anglin-Foote, MHA)

Join VAPheLib ListServ:

VAPHELIB-L@VAWWW.LISTSERV.VA.GOV

Contact Us: VAPheLib@va.gov

Reaching VA-wide | Building Partnerships | Integrating Knowledge | Collaborating

JOIN THE TEAM!

VA Phenomics Library

❖ **Mission:** *To provide an encyclopedia of VHA EHR based phenotyping through **integration of metadata on phenomics work across the VA research and clinical operations community** to optimize VA data use for VA research and clinical operations and to serve the VA community*

❖ Objectives:

- ✓ To provide a knowledgebase framework to collect, store/archive and share phenotype definitions/data mapping/other metadata used in VA projects and publications
- ✓ To expedite VA science by enabling phenotype reusability and scalability across VA projects
- ✓ To build a platform to encourage and enhance collaboration and communication across the VA research community
- ✓ **To collect 1000 curated phenotypes and associated metadata by the end of FY2021**

Office of Research and Development 2019 Priorities

1

Annual Infrastructure Priority

- Ensure that VA research has adequate IT resources

3

Strategic Priorities

- Increase Veterans' access to high quality clinical trials
- Increase the substantial real-world impact of VA research
- Transform VA data into a national resource

5

Cross-Cutting Clinical Priorities

- Gulf War Illness
- Opioids
- PTSD
- Suicide prevention
- Traumatic Brain Injury

Findable/Accessible/Interoperable/Reusable

Wilkinson, M. D. *et al.* The FAIR Guiding Principles for scientific data management and stewardship. *Sci. Data*3:160018 doi: 10.1038/sdata.2016.18 (2016).

VAPheLib – In Perspective

1997

2010

5/30/2017

12/10/2019

4/6/2020

5/12/2020

Boston CSP
Epi Center

MVP launched

MVP ~570K
8 Projects

MVP ~810K
35 Projects



First Phenomics Library (Media Wiki) for MVP
 -The library became a home for MVP's data documentation and shared community resources
 -Wiki platform hosted by VINCI

Kick-off meeting for VA-wide expansion
 -VAPheLib project plan developed

Library opened to VA-wide
 -In support of VA COVID-19 Shared Data Resources

Collection of metadata and building of EHR knowledge
 -VA Research & Clinical Operations Community: conducting research based on ONE BIG VA Cohort
 -20+ years of Boston CSP Epi Center growth and multitudes of research portfolio
 (Similar experiences across the VA)

Key partnerships and content development
 -MVP investigators sharing a wealth of expertise and knowledge on EHR data and phenotyping
 -CSPEAR/VACS/VINCI/others

Reshaping VAPheLib to serve the whole VA research & clinical operations community
 -VAPheLib continues to grow and improve towards becoming part of VA

Reaching VA-wide | Building Partnerships | Integrating Knowledge | Collaborating

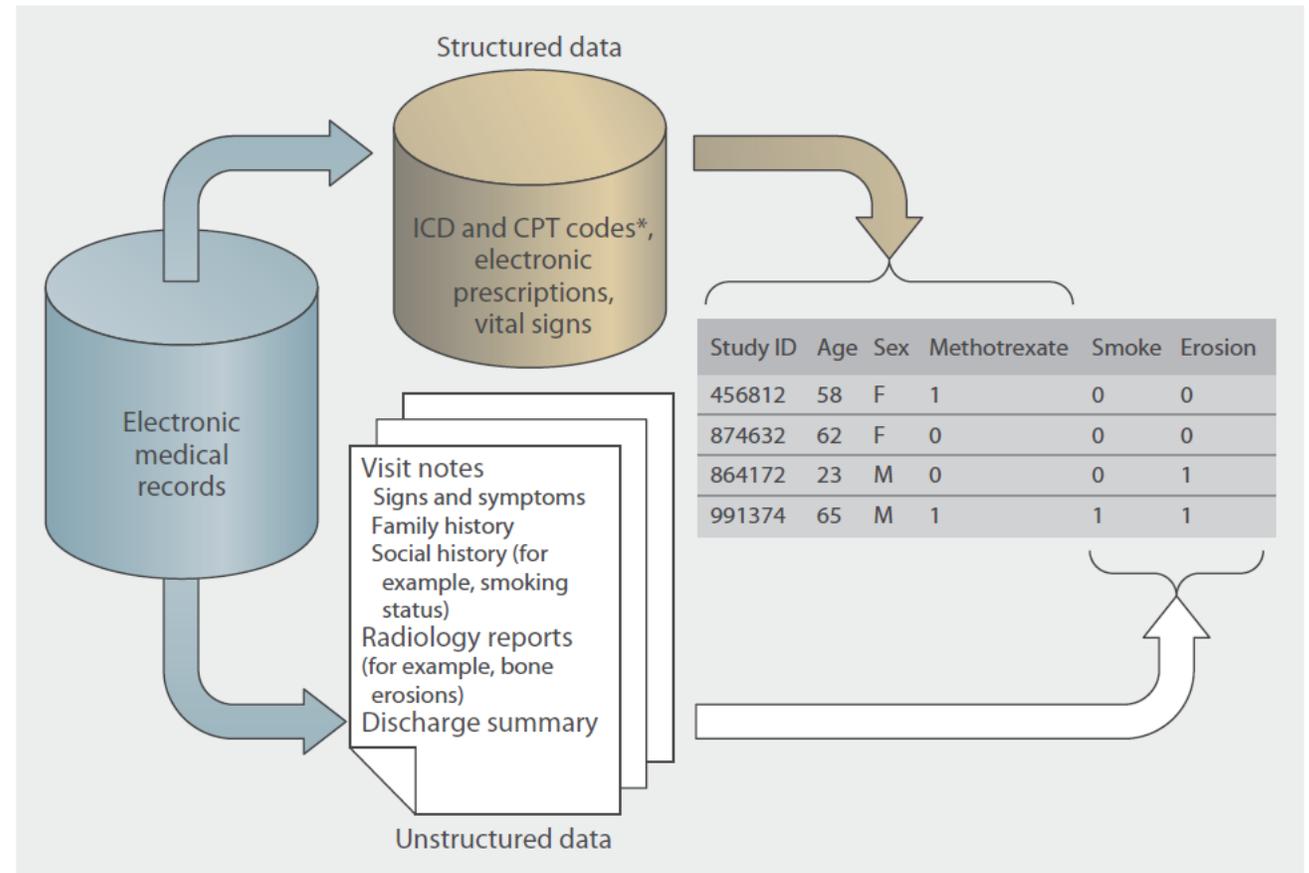
Phenotyping

❖ What is Phenotyping?

- Phenotyping is the process used to identify patients for a condition using data elements of the EMR
- Extract structured data (ICD and CPT codes, electronic prescriptions, vital signs) + unstructured data (clinical notes)

❖ Why is it important?

- Quality clinical data is the key to quality clinical research and translational science.

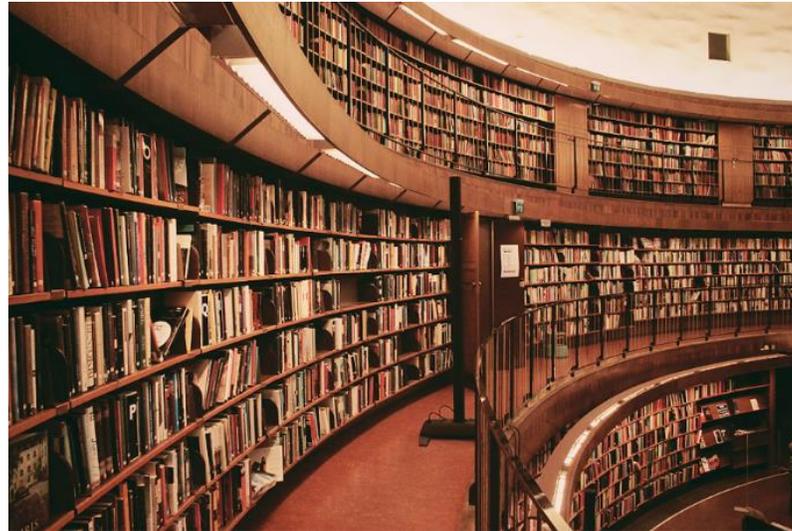


Applied Bioinformatics/High-Throughput Phenotyping Methods
(Liao KP, Sun J, Cai TA, et al. High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. *J Am Med Inform Assoc.* 2019;26(11):1255-1262)

Phenotyping Goals

More and more data are becoming available for research: Is it a blessing or a curse?

- Opportunities and challenges
- Are there appropriate tools and resources to analyze, manage and handle these data?
- Are we optimally synthesizing all the information? How do we find what we are looking for?
- Do we have all the information and annotation?



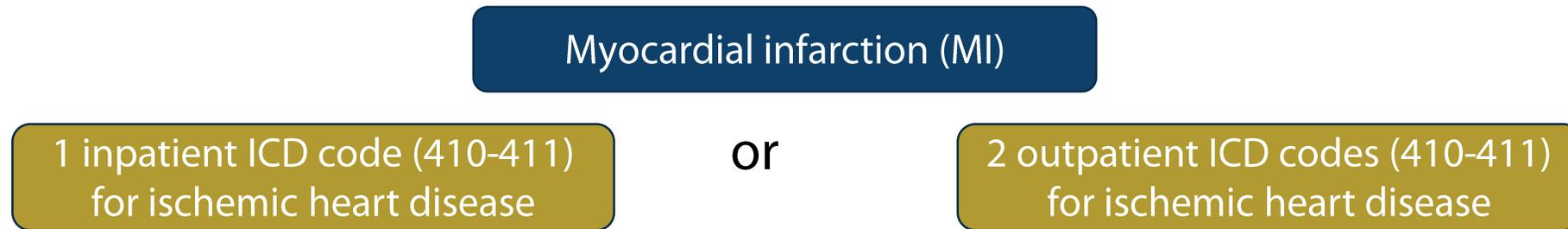
Sometimes, data warehouses resemble landfills more than libraries.

-Phenotypes are the foundation of clinical research

-Major challenge is in accurately and efficiently assigning phenotypes to subjects

Phenotyping – MI Example

- Multiple definitions for EHR-based myocardial infarction (MI) in literature:



- Phenotypes are defined and derived to meet the needs of varying research goals and questions
- Need to understand these metadata and provenance of algorithm developed
- Application:
 - Apply these algorithms to create cohorts of patients; traditional clinical studies can then be performed on these cohorts to understand health care utilization or risk factors for potentially avoidable outcomes

❖ **VAPheLib Goal - Capturing Metadata and Annotation**

❖ **Catalogue of phenotypes used for VA research and clinical operations
to reuse and to continue to build the shared knowledgebase**

VAPheLib - Transition

❖ MVP Phenotype Annotation Library:

- The MVP Data Core initially set-up the library to serve the Million Veteran Program (MVP)

❖ Expansion to VA PHENOMICS LIBRARY:

- At the direction of the CRADO, the MVP library is now expanding to serve the entire VA research and clinical operations community
- Planning meeting for this effort was held in December 2019
- Leadership
 - **MVP/VA Boston Data Core:** Kelly Cho, MPH, PhD
 - **VA Central Office Lead:** Sumitra Muralidhar, PhD
 - **Supported by:** MVP, CSP, VINCI

The screenshot displays the VA Phenomics Library website interface. At the top, there is a navigation bar with 'Main page' and 'Discussion' tabs. The main heading is 'Main Page'. Below this, the website features a sidebar with various navigation options: Data Core (Data Analytics Team, Phenomics Core), Projects (Project Overview), Phenotypes (Phenotypes, Phenotype Forms), Data (Core Data, Other Data Sources, Other Non-CDW Production Files, Datacubes), VA Research Community (VINCI, MAVERIC Informatics), and How to Use Library. The main content area includes the Department of Veterans Affairs seal, another 'Main page' and 'Discussion' navigation bar, and the title 'VA Phenomics Library'. Below the title are links for 'Jump to navigation' and 'Jump to search'. A 'Contents' table of contents lists: 1 Overview, 2 Mission, 3 Objectives, 4 How to, and 5 Contact. The 'Overview' section begins with the text: 'The VA Phenomics Library (VAPheLib) is a shared knowledge resource of the Million Veteran Program (MVP) on behalf of the Office of Research and Development (ORD) that can be used in ORD supported research and for its Studies Program (CSP), and VA Informatics and Computing (I&C)'. The 'Mission' section starts with: 'To provide an encyclopedia of VHA EMR based phenotypes and to serve the VA research community'. At the bottom, a URL is visible: https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/VA_Phenomics_Library.

VAPheLib Project Plan

VA Phenomics Library: Project Plan

Million Veteran Program (MVP) Data Core
CSP Epidemiology Center (CSPEC)

Leads: Kelly Cho & Jackie Honerlaw
ORD: Suma Muralidhar
Supported by: MVP, CSP, VINCI

Revision History:

Version	Date	Author
DRAFT 1.0	January 24 th , 2020	KC, JH

IV. Project Management Plan

A. Project Timeline - Tentative

	FY2020				FY2021			
1. Onboard library staff								
2. Perform Landscape Assessment of VA research community								
3. Integrate feedback from Landscape Assessment into MediaWiki								
4. Open library to VA research community		Timeline Shortened – Open Now						
5. Develop priority phenotypes for VA researcher use								
6. Draft implementation plan for further innovations								

Library opened to VA
on 4/6/2020
-In support of
facilitating
VA COVID-19 Shared
Data Resources

VAPheLib Expansion Progress Continues!

Build Partnerships & Expand Userbase

- Key stakeholders and groups
 - Understand needs
 - Enhance content expertise pool
- Initial focus - published and readily available metadata contribution
- On going – currently active and prospective phenomics work products/phenotypes



Becoming VA Research Resource for Everyday Use



Grow Content, Improve & Innovate

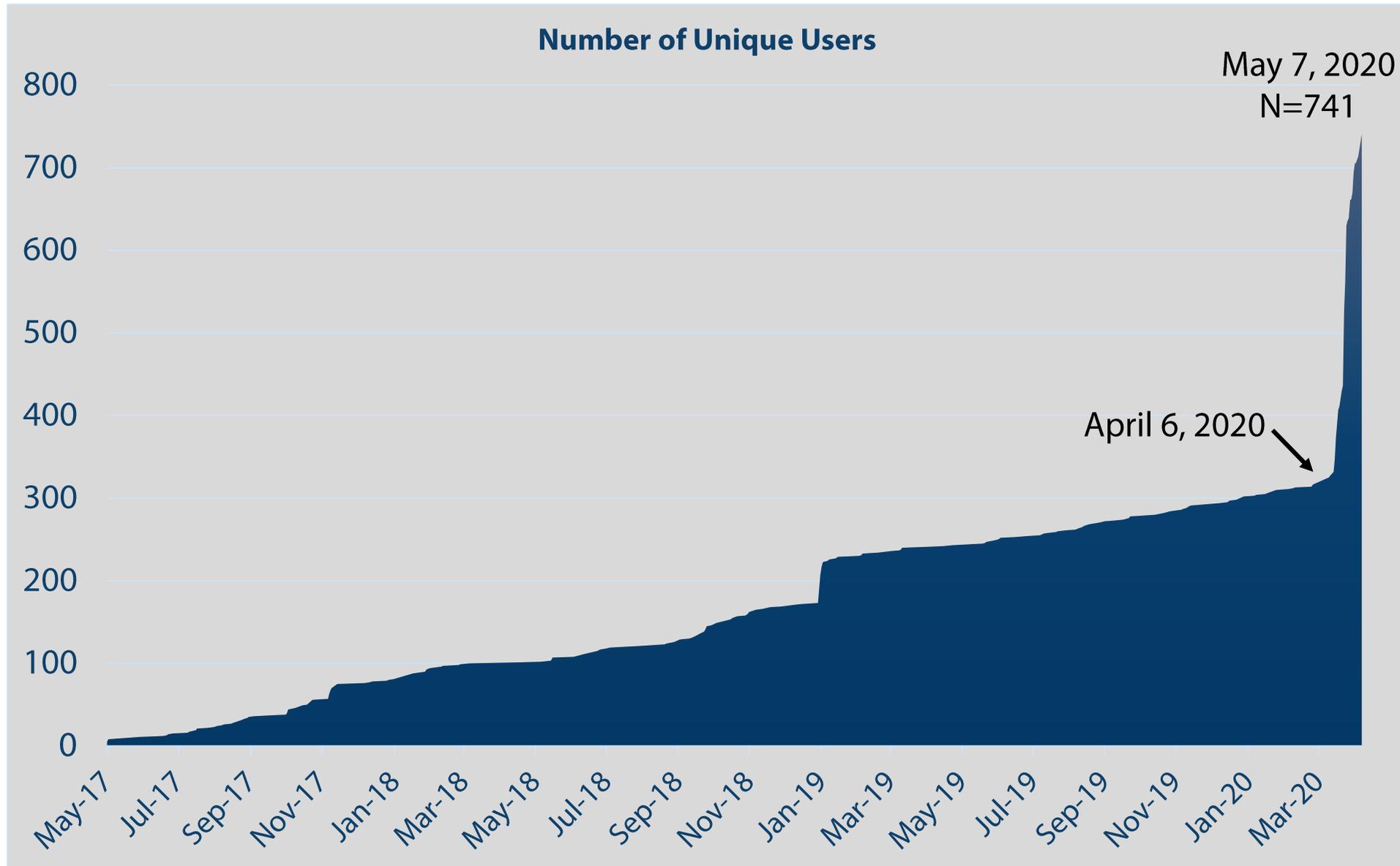
- Integrate feedback
- Improve VAPheLib utility layout/features/extensions
- Increase content collection
- Continue phenotype curation on priority phenotypes
- Further EHR data innovation leverage the VAPheLib knowledgebase
- VA-DOE Collaboration

Reaching VA-wide |
Building Partnerships |
Integrating Knowledge |
Collaborating |

VA PHENOMICS LIBRARY: Current State – May 2020



VAPheLib – Userbase



VAPheLib – Utilization By Station

Top 10 VA Sites

Boston

Salt Lake City

Seattle

Washington

Palo Alto

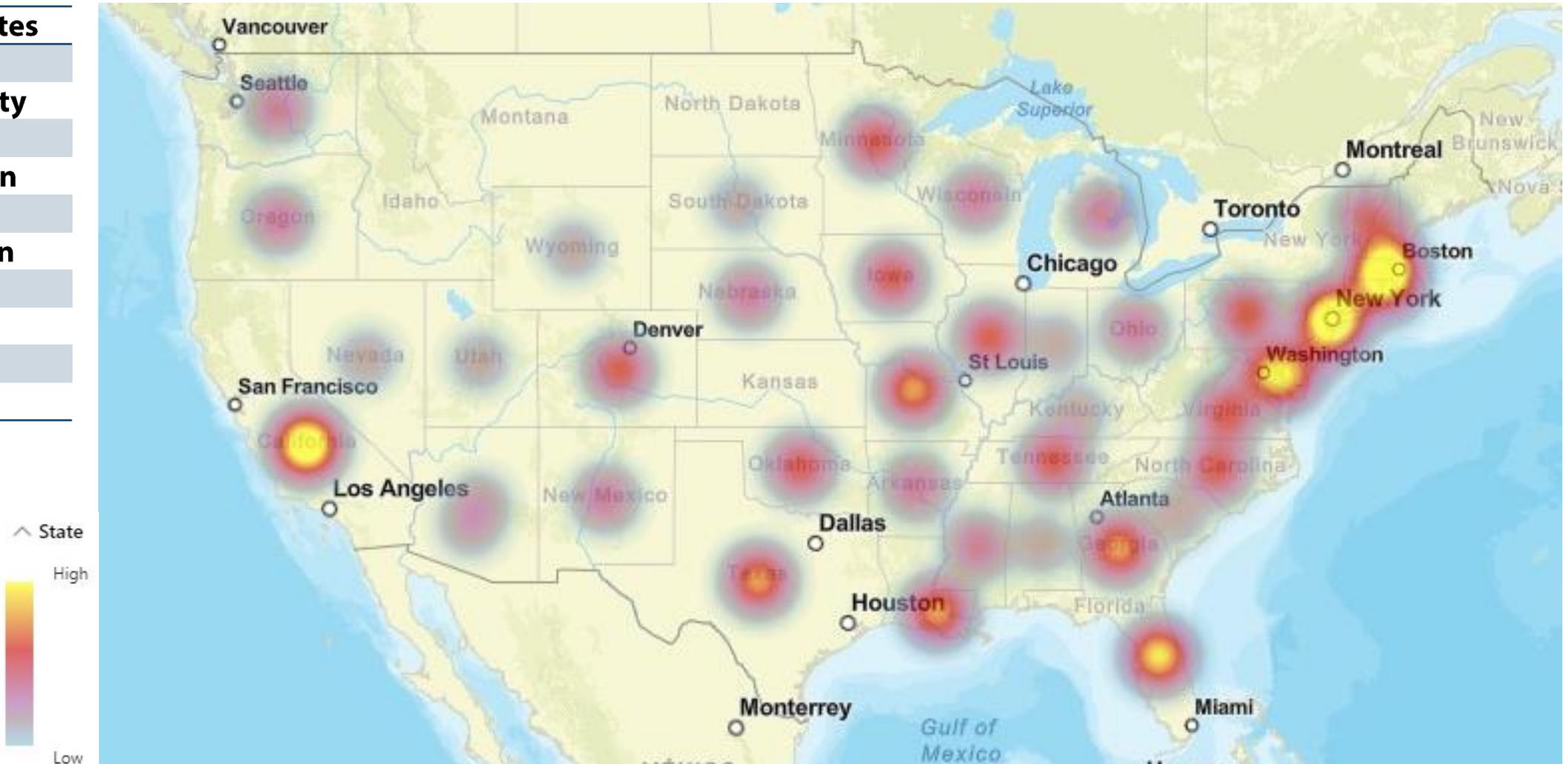
West Haven

Durham

Hines

Bronx

Miami



VAPheLib – Phenomics Data Coverage

Data Classifications	Total Phenotypes
Demographics	7
Vitals	6
Laboratory	77
Medications	52
Procedures	7
Diseases	1,991*
Lifestyle & Environmental Factors	16
Total	2,156**

*Liao KP, Sun J, Cai TA, et al. High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. *J Am Med Inform Assoc.* 2019;26(11):1255-1262. [https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/MAP_\(MVP_Dat acube\)](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/MAP_(MVP_Dat acube))

(Data as of May 8, 2020)

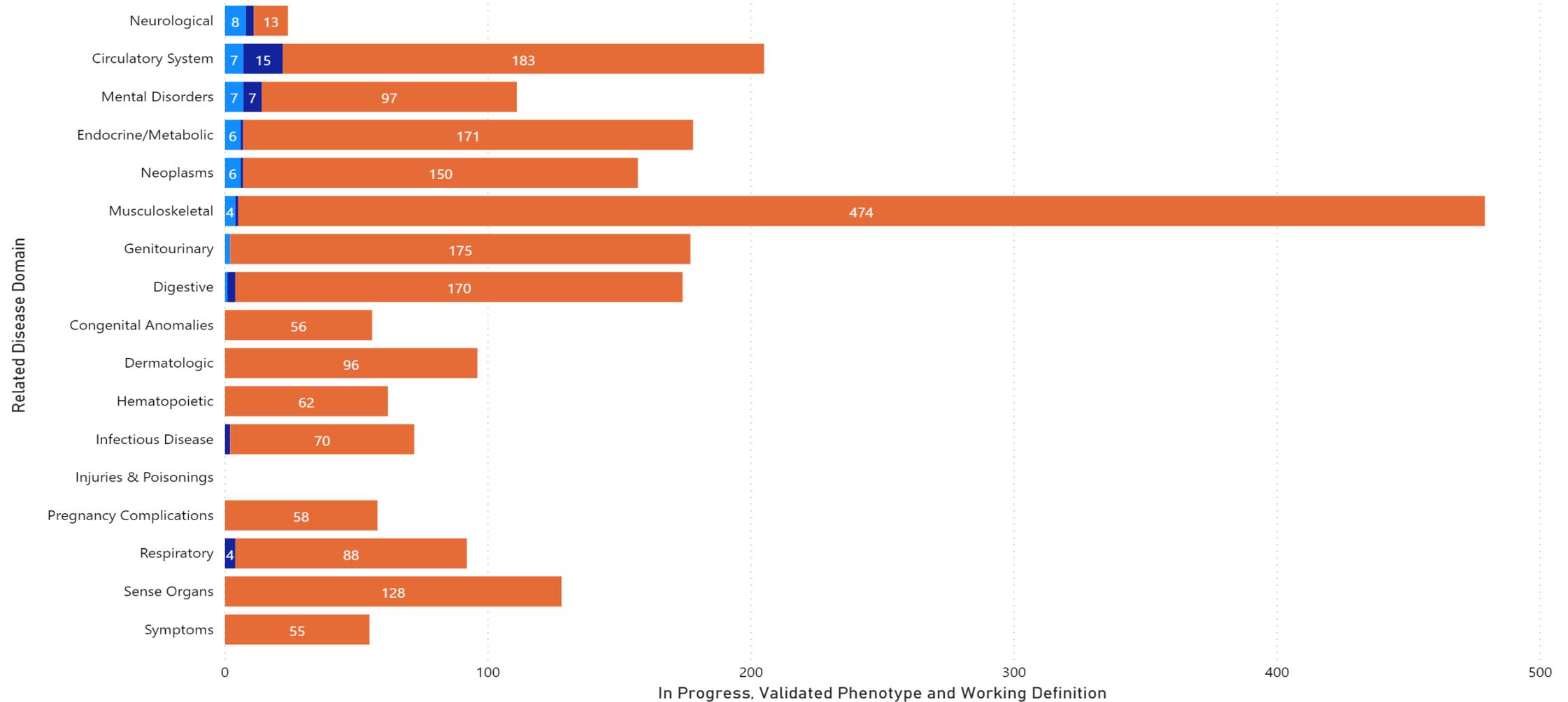
Curation Status
In Progress
Working Definition
Validated Phenotype

- ❖ Phenotypes are collected at various stages of development for various utilities and updated as more information is available
- ❖ **Most of these are “in-progress or working algorithms” and further data curation/validation work is on-going and needed.
- ❖ Currently there are 39 publications on various phenotypes and the number is growing.
 - ✓ Goal – Link to already published VA EHR phenotype work through partnerships

VAPheLib – Phenotype Coverage

In Progress, Validated Phenotype and Working Definition by Related Disease Domain

● In Progress ● Validated Phenotype ● Working Definition





❖ VA PHENOMICS LIBRARY
- Live Demonstration -

Switching to live Library demonstration

https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/VA_Phenomics_Library



❖ VAPheLib Summary &
Next Steps

VAPheLib – Summary

- **VAPheLib**

- Sponsored by VA ORD under Dr. Rachel Ramoni in collaboration with MVP, CSP and VINCI
- Mission: To provide an encyclopedia of VHA EMR based phenotyping through integration of phenomics work from across the VA research and clinical operations community to optimize VA data use for VA research and clinical operations and to serve the VA community
- Open to VA-wide as of April 6, 2020 and is continuously being updated!

- **Expand content & partnership**

- VA priority data domains for metadata
- VA expertise and key stakeholders
- Current and future research needs
- Complement existing VA resources

- **Continue building knowledgebase** - Portable, sharable, scalable

Next Steps

✓ Become a User!

- [https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/VA Phenomics Library](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/VA_Phenomics_Library)
- Please also join our [VAPheLib ListServ](#) by clicking on the link, or send an email to VAPHELIB-L@VAWWW.LISTSERV.VA.GOV to receive frequent updates and be part of ongoing discussions.

✓ Become a Contributor! Become a Partner!

- Join our partners group by contributing and sharing your expertise with VA community
- You can learn more about how to become a contributor:
[https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/How to contribute](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/How_to_contribute)

✓ Feedback – We want to hear from you!

- Contact us at VAPheLib@va.gov :
 - ✓ For more information on the VA Phenomics Library
 - ✓ For suggestions, questions, and comments



Questions?

For any questions, comments, and/or suggestions,

Please contact: VAPheLib@va.gov



Findable
Accessible
Interoperable
Reusable

Wilkinson, M. D. *et al.* The FAIR Guiding Principles for scientific data management and stewardship. *Sci. Data*3:160018 doi: 10.1038/sdata.2016.18 (2016).

❖ *VAPheLib* – Live Demonstration

Key Contents

- ✓ ***Please note: The following slides represent a general content of our live demonstration to be presented. Therefore it may not follow the exact order or level of details.***

Content includes:

- How to navigate VAPheLib Wiki
https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/VA_Phenomics_Library
- Examples of phenotype metadata
- How to contribute



Main page **Discussion**

Read [View source](#) [View history](#) ☆

VA Phenomics Library

[Jump to navigation](#) [Jump to search](#)

Contents

- [Overview](#)
- [Mission](#)
- [Objectives](#)
- [How to](#)
- [Contact](#)

Overview

The VA Phenomics Library (VAPheLib) is a shared knowledgebase of VAEHR-based phenotype Development (ORD). This effort is part of an enterprise-wide approach to provide a resource for the Veteran Program (MVP), Cooperative Studies Program (CSP), and VA Informatics and Computing

Mission

To provide an encyclopedia of VHAEMR based phenotyping through integration of phenomics

Objectives

- To provide a knowledgebase framework to collect, store/archive and share phenotype data
- To expedite VA science by enabling phenotype reusability and scalability across VA projects
- To build a platform to encourage and enhance collaboration and communication across VA projects

How to

Browse phenotypes: Visit the [Phenotype Catalogue](#) to search by domain or use the search bar.
Contribute to the Library: Visit the [Howto contribute](#) page to find how showcase your work.

Contact

About the Library

- [Main page](#)
- [Quick Look](#)
- [VAPheLib Team](#)
- [FAQ](#)

Browsing Content

- [Phenotype Catalogue](#)
- [Data Classifications](#)
- [Disease Domains](#)
- [COVID-19:Shared Data Resource](#)
- [Publications](#)

How do I contribute?

- [How to contribute](#)
- [Phenotype Entry Form](#)
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Contributors and Partners

- [MVP](#)
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- [VINCI](#)
- [Other Investigators and Groups](#)

Tools

- [What links here](#)
- [Related changes](#)
- [Upload file](#)

About the Library

- [Main page](#)
- [Quick Look](#)
- [VAPheLib Team](#)
- [FAQ](#)

Browsing Content

- [Phenotype Catalogue](#)
- [Data Classifications](#)
- [Disease Domains](#)
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- [VINCI](#)
- [Other Investigators and Groups](#)

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- [What links here](#)
- [Related changes](#)
- [Upload file](#)

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Main page [Discussion](#)

VA Phenomics Library

[Jump to navigation](#) [Jump to search](#)

Contents

- [Overview](#)
- [Mission](#)
- [Objectives](#)
- [How to](#)
- [Contact](#)

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Contact

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19 Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype EntryForm](#)
[Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

[MVP](#)
[CSPEAR](#)
[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)



VA PHENOMICS LIBRARY

VAPheLib
04/27/2020[View history](#)

What is the VA PHENOMICS LIBRARY?

- ❖ The VA PHENOMICS LIBRARY (VAPheLib) is a national Office of Research and Development initiative launched in December 2019 with the goal to catalog 1000 phenotypes by the end of 2021.
- ❖ The VAPheLib establishes a catalog of curated phenotypes and associated metadata needed to reproduce electronic medical record-based phenotype definitions.
- ❖ The library serves as a central location for contributing, sharing and browsing content curated by VA researchers and clinical stakeholders.

What content is stored in the library?

- ✓ Algorithm Description
- ✓ Data Mappings
- ✓ Validation Process
- ✓ Data Sources Used
- ✓ Citation
- ✓ Author Contact
- ✓ Links to Useful Resources

The screenshot shows the VA Phenomics Library website interface. It includes a navigation menu with links for Overview, Mission, Objectives, How to, and Contact. Below the menu, there is a 'Mission' section with a paragraph of text and a list of objectives. The 'How to' section includes links for 'Browse phenotypes' and 'Contribute to the Library'. The 'Contact' section provides an email address for inquiries.

What are the benefits of a centralized phenomics library?

- ❖ Provides a knowledge base framework to collect, store, archive and share phenotype definitions, data mapping and other metadata used in VA projects and publications.
- ❖ Facilitates sharing of phenotype definitions improving reusability and scalability of information across VA projects and provides a platform to enhance collaboration and communication across the VA research and clinical communities.
- ❖ Expedites VA science by serving as a ready resource to define eligible cases for VA research such as clinical trials or epidemiological studies.

Who do I contact for more information?

Email VAPheLib@va.gov for:

- ✓ General questions
- ✓ Access to library
- ✓ Library demonstration
- ✓ Submission of phenotypes


[Main page](#)
[Discussion](#)

VA Phenomics

[Jump to navigation](#)
[Jump to search](#)

Contents

- [Overview](#)
- [Mission](#)
- [Objectives](#)
- [How to](#)
- [Contact](#)

Overview

The VA Phenomics Library (VAPheLib) is sponsored by the Million Veteran Program (MVP) on behalf of the Office of Research and Development (ORD) and the Million Veteran Program (MVP), Cooperative Studies Program (CSP), and VINCI.

Mission

To provide an encyclopedia

Objectives

- To provide a knowledgebase
- To expedite VA scientific research
- To build a platform to

How to

Browse phenotypes: [VAPheLib](#)
Contribute to the Library: [VAPheLib](#)

Contact

VAPheLib Team

[Jump to navigation](#)
[Jump to search](#)

The VA Phenomics Library (VAPheLib) is sponsored by the Million Veteran Program (MVP) on behalf of the Office of Research and Development (ORD) and the Million Veteran Program (MVP), Cooperative Studies Program (CSP), and VINCI.

Contributors and Partners

The content of this knowledgebase is a collective work across many VA research groups and investigators. We truly appreciate their valuable contribution and partners can be found from each link below [Contributors and Partners](#). In addition to these key contributors, VAPheLib team has been building new contributors and partners list is growing each day, and we will continue to update this page with more information. Thank you for joining the VAPheLib Team.

Join VAPheLib Team

We invite every VA investigator to join this partnership and get frequent updates and reports. You can learn more about how to become a [contributor](#). Please email VAPheLib@VAWWW.LISTSERV.VAGOV to receive frequent updates and be part of ongoing discussions.

VAPheLib Program Team

VACO Lead: Sumitra Muralidhar, Ph.D

Director: Kelly Cho, Ph.D, MPH

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Contact us at VAPheLib@va.gov

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COMD-19 Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype Entry Form](#)
[Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

[MVP](#)
[CSPEAR](#)
[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)


[Main page](#) [Discussion](#)

VA Phenomics Libr

[Jump to navigation](#) [Jump to search](#)

Contents

- [Overview](#)
- [Mission](#)
- [Objectives](#)
- [How to](#)
- [Contact](#)

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Mission

To provide an encyclopedia of VHAEM

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Contact

Frequently Asked Questions

[Jump to navigation](#) [Jump to search](#)

Contents

- [How do I navigate the VA Phenomics Library?](#)
- [How do I contribute content to the library?](#)
- [How do I search phenotypes? Are all the phenotypes available in the VA Phenomics Library Validated?](#)
- [How do I use the information available in the library for my own study?](#)
- [What should I do if I need data that is not already provided for my study?](#)
- [Information regarding the Million Veteran Program \(MVP\), does this mean I can use MVP data for my study?](#)
- [How do I get more involved with the VA Phenomics Library?](#)

How do I navigate the VA Phenomics Library?

The [Main Page](#) provides a brief overview of the library and the data available within the library. To search for specific phenotypes please follow the instruction and links in the "How To" section of the Main Page.

How do I contribute content to the library?

Please refer to the [How to contribute](#) page for more information.

How do I search phenotypes? Are all the phenotypes available in the VA Phenomics Library Validated?

To see if a phenotype currently exists for the classification or related disease domain you are interested in, you can either navigate to the [Main Page](#), or you can use the search box in the upper right hand corner of the page. Once on specific page for your phenotype of interest, you can use the search box in the upper right hand corner of the page. Additionally, each phenotype within the VAPheLib is categorized by status (In Progress, Working Definition, and Validated). To see if a phenotype is validated, you can navigate to the [Phenotype Catalogue](#) page and choosing the status of interest.

How do I use the information available in the library for my own study?

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19 Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype EntryForm](#)
[Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

[MVP](#)
[CSPEAR](#)
[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)

Page [Discussion](#)

Phenotype Overview

[Jump to navigation](#) [Jump to search](#)

Contents

- [1 Status](#)
- [2 Published Phenotypes](#)
- [3 Data Classifications](#)
- [4 Disease Domains](#)
- [5 Contributors and Partners](#)

Status

- In Progress:** Phenotypes in development
- Working Definition:** Phenotypes that are completed, but not validated
- Validated Phenotype:** Completed and validated phenotypes

Published Phenotypes

Data Classifications

- [Demographics](#)
- [Vitals](#)

Data Classifications

- [Demographics](#)
- [Vitals](#)
- [Laboratory](#)
- [Medications](#)
- [Procedures](#)
- [Diseases](#)
- [Lifestyle/Environmental Factors](#)

Disease Domains

- [Circulatory System](#)
- [Congenital Anomalies](#)
- [Dermatologic](#)
- [Digestive](#)
- [Endocrine/Metabolic](#)
- [Genitourinary](#)
- [Hematopoietic](#)
- [Infectious Disease](#)
- [Injuries & Poisonings](#)
- [Mental Disorders](#)
- [Musculoskeletal](#)
- [Neoplasms](#)
- [Neurological](#)
- [Pregnancy Complications](#)
- [Respiratory](#)

❖ Browsing Tips

- **Search by Data Classifications, Disease Domains or Status type**
- **Check out list of publications currently catalogued**

About the Library

- [Main page](#)
- [Quick Look](#)
- [VAPheLib Team](#)
- [FAQ](#)

Browsing Content

- [Phenotype Catalogue](#)
- [Data Classifications](#)
- [Disease Domains](#)
- [COVID-19: Shared Data Resource](#)
- [Publications](#)

How do I contribute?

- [How to contribute](#)
- [Phenotype Entry Form](#)
- [Subscribe to the VAPheLib ListServ](#)

Contributors and Partners



Page [Discussion](#)

Phenotype Overview

[Jump to navigation](#) [Jump to search](#)

Contents

- [Status](#)
- [Published Phenotypes](#)
- [Data Classifications](#)
- [Disease Domains](#)
- [Contributors and Partners](#)

Status

- [In Progress: Phenotypes in development](#)
- [Working Definition: Phenotypes that are under review](#)
- [Validated Phenotype: Completed and ready for use](#)

Published Phenotypes

Data Classifications

- [Demographics](#)
- [Vitals](#)
- [Laboratory](#)
- [Medications](#)
- [Procedures](#)
- [Diseases](#)**
- [Lifestyle/Environmental Factors](#)

Disease Domains

- [Circulatory System](#)
- [Congenital Anomalies](#)

Category:Diseases

[Jump to navigation](#) [Jump to search](#)

[Top](#) [A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#)

Pages in category "Diseases"

The following 200 pages are in this category, out of 200 total pages (previous page) (next page)

A

- [Abdominal aortic aneurysm \(MAP\)](#)
- [Abdominal hernia \(MAP\)](#)
- [Abdominal pain \(MAP\)](#)
- [Abnormal arterial blood gases \(MAP\)](#)
- [Abnormal chest sounds \(MAP\)](#)
- [Abnormal coagulation profile \(MAP\)](#)
- [Abnormal electrocardiogram \(ECG\) \(EKG\) \(MAP\)](#)
- [Abnormal findings examination of lungs \(MAP\)](#)
- [Abnormal findings on examination of urine \(MAP\)](#)
- [Abnormal findings on exam of gastrointestinal tract \(MAP\)](#)
- [Abnormal findings on mammogram or breast exam \(MAP\)](#)
- [Abnormal findings on study of brain and-or nerves \(MAP\)](#)
- [Abnormal function study of cardiovascular system \(MAP\)](#)
- [Abnormal glucose \(MAP\)](#)
- [Abnormal granulation tissue \(MAP\)](#)
- [Abnormal heart sounds \(MAP\)](#)
- [Abnormal involuntary movements \(MAP\)](#)
- [Abnormality in fetal heart rate or rhythm \(MAP\)](#)
- [Abnormality of gait \(MAP\)](#)
- [Abnormality of organs and soft tissues of pelvis \(MAP\)](#)

M

- [Macroglobulinemia \(MAP\)](#)
- [Macular degeneration, dry \(MAP\)](#)
- [Macular degeneration \(senile\) of retina \(MAP\)](#)
- [Macular degeneration, wet \(MAP\)](#)
- [Macular puckering of retina \(MAP\)](#)
- [Major depressive disorder \(MAP\)](#)
- [Major puerperal infection \(MAP\)](#)
- [Malaise and fatigue \(MAP\)](#)
- [Male infertility and abnormal spermatozoa \(MAP\)](#)
- [Malignant neoplasm of bladder \(MAP\)](#)
- [Malignant neoplasm of female breast \(MAP\)](#)
- [Malignant neoplasm of gallbladder and biliary tract \(MAP\)](#)
- [Malignant neoplasm of kidney, except papillary cell carcinoma \(MAP\)](#)
- [Malignant neoplasm of liver, primary \(MAP\)](#)
- [Malignant neoplasm of other and ill-defined sites of digestive system \(MAP\)](#)
- [Malignant neoplasm of other urinary organs \(MAP\)](#)
- [Malignant neoplasm of ovary and other female genital organs \(MAP\)](#)
- [Malignant neoplasm of ovary \(MAP\)](#)
- [Malignant neoplasm of rectum, rectosigmoid junction \(MAP\)](#)
- [Malignant neoplasm of renal pelvis \(MAP\)](#)
- [Malignant neoplasm of retroperitoneum \(MAP\)](#)
- [Malignant neoplasm of small intestine \(MAP\)](#)
- [Malignant neoplasm of testis \(MAP\)](#)
- [Malignant neoplasm of unspecified male genital organs \(MAP\)](#)
- [Malignant neoplasm of uterus \(MAP\)](#)
- [Malignant neoplasm, other \(MAP\)](#)
- [Malposition and malpresentation of fetus \(MAP\)](#)
- [Malunion and nonunion of fracture \(MAP\)](#)
- [Mammographic microcalcification \(MAP\)](#)
- [Malignant and unknown neoplasms of unspecified sites \(MAP\)](#)
- [Mastodynia \(MAP\)](#)
- [Mood disorders \(MAP\)](#)
- [Morbid obesity \(MAP\)](#)
- [Moyamoya disease \(MAP\)](#)
- [MRSA pneumonia \(MAP\)](#)
- [Mucous polyp of cervix \(MAP\)](#)
- [Multiple gestation \(MAP\)](#)
- [Multiple Myeloma](#)
- [Multiple myeloma \(MAP\)](#)
- [Multiple sclerosis \(MAP\)](#)
- [Muscle-tendon sprain \(MAP\)](#)
- [Muscle weakness \(MAP\)](#)
- [Muscular calcification and ossification \(MAP\)](#)
- [Muscular dystrophies and other myopathies \(MAP\)](#)
- [Muscular dystrophies \(MAP\)](#)
- [Muscular wasting and disuse atrophy \(MAP\)](#)
- [Musculoskeletal symptoms referable to limbs \(MAP\)](#)
- [Myalgia and myositis unspecified \(MAP\)](#)
- [Myasthenia gravis \(MAP\)](#)
- [Mycoses \(MAP\)](#)
- [Myelofibrosis \(MAP\)](#)
- [Myeloid leukemia, acute \(MAP\)](#)
- [Myeloid leukemia, chronic \(MAP\)](#)
- [Myeloid leukemia \(MAP\)](#)
- [Myeloproliferative disease \(MAP\)](#)
- [Myocardial Infarction/Coronary Artery Disease \(VACS\)](#)
- [Myocardial infarction \(MAP\)](#)
- [Myocardial Infarction MI \(SAFE\)](#)
- [Myocarditis \(MAP\)](#)
- [Myodonus \(MAP\)](#)
- [Myoneural disorders \(MAP\)](#)
- [Myopathy \(MAP\)](#)
- [Myopia \(MAP\)](#)
- [Myringitis \(MAP\)](#)

[https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Myocardial_Infarction_MI_\(SAFE\)](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Myocardial_Infarction_MI_(SAFE))

Myocardial Infarction MI (SAFE)

[Jump to navigation](#) [Jump to search](#)**Phenotype:** Myocardial Infarction (MI)**PhenotypeID:** 00023**Status:** Validated Phenotype

Contents

- [1 Phenotype Table](#)
- [2 Algorithm Overview](#)
- [3 Publication](#)
- [4 Algorithm Components](#)
- [5 Validation](#)
- [6 Source of Phenotype Data](#)

Phenotype Table

Value: Yes, No

"Yes": Value_Probability >= 0.758 (Pat

"No": Value_Probability < 0.758

Value_Probability: 0-1

This algorithm yields the probability that a patient has ever had an MI.

Algorithm Overview

Classification: [Diseases](#)**Related Disease Domain:** [Circulatory System](#)**Algorithm Description:** The SAFE method uses structure

1. Application of broad ICD code filter to identify possible MI patients using CDW and CMS data. If a patient only had an MI diagnosis in the CDW data pass this set met the filter criteria.
2. Select features for model training including relevant ICD codes only used for the filter. Create MI dictionary by majority class.
3. Model training with gold standard labels.

Final model (after orthogonalizing the features): $\text{logit Pr}(MI) = 0.5419398 * \log(1 + C0002962) - 0.6731429 * \log(1 + No)$ **Population:** All VA users.**Date Algorithm Created:** June 2019**Author:** [CVD Merit](#)**Contact:** Anne Ho (Yuk-Lam.Ho@va.gov)

Publication

Description of SAFE method: Yu S, Chakraborty A, Liao KP, et al. Surrogate-as

Algorithm Components

main_icd	410.X, 412.X (ICD-9) I21.X, I22.X, I25.2 (ICD-10)
ihd_icd	410.X, 411.X, 412.X, 414.X (ICD-9) I20.0, I21.X, I22.X, I24.X I25.2
C0027051	Myocardial_Infarction CUI
C0002962	Angina Pectoris CUI
Note_Count	Total count of notes per patient

Validation

Algorithm Validation: Performed**Description of Validation:** 100 random charts reviewed to determine prevalence of MI.**Algorithm Performance Measures:** AUC for validation set: 0.871 (Possible MI)

If the probability is cut at 0.758, the model achieves PPV of 0.908 and NPV of 0.871. Assuming that the filter negative patients don't have MI, the model achieves p

Source of Phenotype Data

Data Sources Used:

Corporate Data Warehouse (CDW)
 CMS data
 TIU Notes

Role of Phenotype in Analysis: Primary Outcome / Exposure[Categories:](#) [Diseases](#) | [Circulatory System](#) | [CVD Merit](#) | [PhenotypeID Assigned](#)



Special page

Search results

[Jump to navigation](#) [Jump to search](#)[Content pages](#) [Multimedia](#) [Everything](#) [Advanced](#)Create the page "**411**" on this wiki! See also the search results found.

[Ischemic Heart Disease \(MAP\)](#)

|Phe411 ...V45_82, 414_1, 414_10, 414_11, 414_12, 414_19, 414_, 414_8, 414_9, 411_8, 411_89 (ICD9): (ICD10)

6 KB (677 words) - 13:05, 4 February 2020

[Other acute and subacute forms of ischemic heart disease \(MAP\)](#)

|Phe411_9 |411_8, 411_89 (ICD9):I24.8, I24.9 (ICD10)

4 KB (539 words) - 13:05, 11 February 2020

[Myocardial Infarction MI \(SAFE\)](#)

...Application of broad ICD code filter to identify possible MI cases: 410.X, 411.X, 412.X (ICD-9); I20.0, I21.X, I22.X, I24.X, I25.110, I25.2, I25.7X0 (ICD-|410.X, 411.X, 412.X, 414.X (ICD-9) I20.0, I21.X, I22.X, I24.X I25.X (ICD-10)

4 KB (524 words) - 10:46, 10 May 2020

[Myocardial Infarction/Coronary Artery Disease \(VACS\)](#)

|410.x, 411.x, 412, 413.x, 429.7, V45.81, V45.82

2 KB (225 words) - 13:41, 6 December 2019

[Cardiovascular Disease \(VINCI\)](#)

OR ICD9Code LIKE '411%'

[Myocardial Infarction/Coronary Artery Disease \(VACS\)](#)

|410.x, 411.x, 412, 413.x, 429.7, V45.81, V45.82

2 KB (225 words) - 13:41, 6 December 2019

[Cardiovascular Disease \(VINCI\)](#)

OR ICD9Code LIKE '411%'

4 KB (621 words) - 14:18, 10 March 2020

[Primary biliary cirrhosis \(MAP\)](#)

|411

4 KB (501 words) - 14:15, 6 February 2020

[Unstable angina \(intermediate coronary syndrome\) \(MAP\)](#)

|Phe411_1 |411_1 (ICD9):I25.700, I25.790, I25.110, I25.730, I25.760, I25.720, I25.710, I25

4 KB (528 words) - 14:15, 6 February 2020

[Coronary atherosclerosis \(MAP\)](#)

|Phe411_4 |411_81, 414_0, 414_00, 414_01, 414_02, 414_03, 414_04, 414_05, 414_2, 414_3, 41

5 KB (620 words) - 13:05, 4 February 2020

[Myocardial infarction \(MAP\)](#)

|Phe411_2 ..._71, 410_72, 410_8, 410_80, 410_81, 410_82, 410_9, 410_90, 410_91, 410_92, 411_0, 412_, 429_7, 429_71, 429_79 (ICD9):I23.6, I23.3, I21, I25.2, I23.2, I22.

5 KB (584 words) - 13:05, 11 February 2020

[Map.usp Conditions](#)

,(4,1,'ICD','411.%') ,(4,2,'ICD','411.%')

191 KB (20,970 words) - 11:41, 22 September 2017

❖ Browsing Tips

- All VAPheLib page text is searchable.
- A search for ICD-9 code 411 (Intermediate coronary syndrome) shows that there are 10 phenotypes that use this code in the definition

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19:Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype EntryForm](#)
[Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

[MVP](#)
[CSPEAR](#)
[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[Upload file](#)
[Special pages](#)
[Printable version](#)

Page [Discussion](#)

Phenotype Overview

[Jump to navigation](#) [Jump to search](#)

Contents

- [Status](#)
- [Published Phenotypes](#)
- [Data Classifications](#)
- [Disease Domains](#)
- [Contributors and Partners](#)

Status

[In Progress](#): Phenotypes in development[Working Definition](#): Phenotypes that are complete[Validated Phenotype](#): Completed and validated phenotype

Published Phenotypes

Data Classifications

[Demographics](#)[Vitals](#)[Laboratory](#)[Medications](#)[Procedures](#)[Diseases](#)[Lifestyle/Environmental Factors](#)

Disease Domains

[Circulatory System](#)[Congenital Anomalies](#)

Category:Medications

[Jump to navigation](#) [Jump to search](#)

Pages in category "Medications"

The following 52 pages are in this category, out of 52 total.

A

[ACE Inhibitors \(Class\)](#)
[Alpha Blockers \(Class\)](#)
[Androgen Deprivation Therapy](#)
[Angiotensin II Inhibitor \(Class\)](#)
[Antianginals \(Class\)](#)
[Anticoagulants \(Class\)](#)
[Antihypertensive Combinations \(Class\)](#)
[Antihypertensive Medications \(Nashville\)](#)
[Antihypertensives, other \(Class\)](#)
[Antilipemic Agents \(Class\)](#)
[Aspirin](#)
[Asthma Medications](#)

B

[Beta Blockers \(Class\)](#)

C

[Cabazitaxel \(MNCI\)](#)
[Calcium Channel Blockers \(Class\)](#)
[Carbonic Anhydrase Inhibitor Diuretics \(Class\)](#)
[Chemotherapy Medications \(MNCI\)](#)
[COPD Medications](#)

H

[Heart Failure Medications](#)
[Hepatitis C Medications](#)
[Highest Morphine Equivalent Daily Dose \(MEDD\) for chronic pain treatment](#)
[HIV Medications](#)
[Hypoglycemic Agents, Other \(Class\)](#)
[Hypothyroid Medications \(MNCI\)](#)

I

[Insulin \(Class\)](#)
[Insulin Medication \(MNCI\)](#)

L

[Leuprolide \(MNCI\)](#)
[Loop Diuretics \(Class\)](#)

M

[MEDD Phenotypes](#)
[Medication Persistence \(VACS\)](#)
[Medications SOP, MNCI](#)
[Mental Health Medications](#)
[Morphine Equivalent Daily Dose \(MEDD\) during inpatient stay hip and knee arthroplasty](#)

O

[Oral Hypoglycemic Agents \(Class\)](#)

P

[Patiromer \(Veltassa\) Medication \(MNCI\)](#)
[Peripheral Vasodilators \(Class\)](#)
[Platelet Aggregation Inhibitors \(Class\)](#)
[Potassium Sparing/Combination Diuretics \(Class\)](#)
[Psychiatric Medications \(MNCI\)](#)
[Pulmonary Fibrotic Disease Medications](#)

S

[Statins](#)

❖ Browsing Tips

- Medication data used for various projects/cohorts and purposes

Antihypertensive Medications (Nashville)

[https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Antihypertensive_Medications_\(Nashville\)](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Antihypertensive_Medications_(Nashville))[Jump to navigation](#) [Jump to search](#)

Contents

- 1 [Phenotype](#)
- 2 [Algorithm Description:](#)
- 3 [Population:](#)
- 4 [Author:](#)
- 5 [Contact:](#)
- 6 [Contact Email:](#)
- 7 [Purpose of Review:](#)

Phenotype

Anti-Hypertensive Medications

Algorithm Description:

List of Anti Hypertensive Medications by class. This

```

WITH HYPERTENSION_COMBO_MEDS
AS
(SELECT
LocalDrugSID,
LocalDrugNameWithDose,
DrugClass,
CASE
WHEN combo_drug_1 IN ('HYDROCHLOROTHIAZ
WHEN combo_drug_1 IN ('CAPTOPRIL',

```

```

WHEN COMBO_DRUG_3 IN ('HYDRALAZINE', 'METHYLDOPA', 'CLONIDINE') THEN 'VASODILATOR'
END AS DRUG_CLASS_3
FROM
(select LocalDrugSID,
LocalDrugNameWithDose,
DrugNameWithoutDose,
DrugClass,
substring(DrugNameWithoutDose,1, (charindex('/', DrugNameWithoutDose,1)-1)) combo_drug_1,
reverse(substring(reverse(DrugNameWithoutDose), 1, (charindex('/', reverse(DrugNameWithoutDose),1)-1))) combo_drug_2,
null as combo_drug_3
from CDWork.dim.LocalDrug
where drugclass = 'CV400'
and len(drugnamewithoutdose) - len(replace(drugnamewithoutdose, '/', '')) = 1
union
select
LocalDrugSID,
LocalDrugNameWithDose,
DrugNameWithoutDose,
DrugClass,
substring(DrugNameWithoutDose, 1, (charindex('/', DrugNameWithoutDose,1)-1)) combo drug 1,
substring(DrugNameWithoutDose,
reverse(substring(reverse(DrugN
from CDWork.dim.LocalDrug
where drugclass = 'CV400'
and len(drugnamewithoutdose) -
)
, tab_columns as
(select
LocalDrugSID,
localdrugnamewithdose,
DRUGCLASS,
DRUG_CLASS_1,
DRUG_CLASS_2,
DRUG_CLASS_3
from HYPERTENSION_COMBO_MEDS)
select
LocalDrugSID,

```

Population:

All VA Users

Author:

MVP Core

Contact:

Otis Wilson

Contact Email:

Otis.Wilson@VA.gov

Purpose of Review:

CDW query to identify Anti-Hypertensive medications including combo medications to prevent double counting by drug classes.

Category: [Medications](#)

❖ Browsing Tips

- Metadata contain scripts/codes for reusing, population, purpose of use, project used, and contributor contact



Category **Discussion**

Category: Lab

[Jump to navigation](#) [Jump to](#)

Pages in category "

The following 77 pages are

A

- [ALT](#)
- [AST](#)

B

- [Basophil](#)
- [Beta-Hydroxybutyrate](#)
- [Bicarbonate](#)

Bilirubin

- [Blood Type \(Boston\)](#)
- [Blood Type \(MNCI\)](#)

BNP

BUN

C

- [CCP](#)
- [CK](#)
- [CKMB](#)
- [Clostridium Difficile \(C. D](#)
- [C-peptide](#)
- [Creatine Kinase \(MNCI\)](#)
- [CRP](#)

Labs Adjudicated

The following labs have been adjudicated

Shortname	Calcium - BSP	MCHC	Mean Corpuscular Hemoglobin Concentration (MCHC)	Brain Natri
A1C	C-peptide	MCV	Mean Corpuscular Volume (MCV)	SA)
ABO Type	CCP	Mg - BSP	Serum Magnesium	
Albumin	Chloride - BSP	Microalbumin	Microalbumin	(RDW)
ALT	CKMB - Abs	Microalbumin Point	Microalbumin	
AST	CKMB - Fra	Microalbumin Spot	Microalbumin	
Baso - Abs	Creat - BSP	Microalbumin Urine 24h	Microalbumin	
Baso - Fra	CRP	Microalbumin Urine Rand	Microalbumin	
Bicarbonate	eGFR	Microalbumin Urine Rand~REFERENCE	Microalbumin	
Bilirubin	Eos - Abs	Microalbumin/Creatinine	Microalbumin	
Bilirubin Crystals	Eos - Fra	Microalbumin/creatinine ratio	Microalbumin	
Bilirubin Delta	ESR	Microalbumin/Creatinine~24HR	Microalbumin	
Bilirubin Direct	GAD	Mono - Abs	Monocyte - Absolute Value	
Bilirubin Indirect	Glucose	Mono - Fra	Monocyte - Fractional Value	
Bilirubin Qual Feces	Glucose - Fasting	MPV	Mean Platelet Volume (MPV)	
Bilirubin Stick	Glucose - FS	Neut - Abs	Neutrophil - Absolute Value	
Bilirubin Total	HCV - Ab	Neut - Fra	Neutrophil - Fractional Value	
Bilirubin Total and Direct	HCV - RNA VL	Phosphatase Alkaline	Phosphatase Alkaline	
Bilirubin Unconjugated	HCV - bDNA VL	Phosphatase Alkaline (Specialty L	Phosphatase Alkaline	
Calculus Comp Calcium Bilirubin	HCV - Genotype	Phosphatase Alkaline Bone	Phosphatase Alkaline	
BNP	HDLC	Phosphatase Alkaline Heat Labile	Phosphatase Alkaline	
BOHB	Hemoglobin	Phosphatase Alkaline Heat Stable	Phosphatase Alkaline	
BUN - BSP	INR	Phosphatase Alkaline Intestine	Phosphatase Alkaline	
Calcium - BSP	Insulin Ab	Phosphatase Alkaline Isoenz	Phosphatase Alkaline	
C-peptide	LDLC	Phosphatase Alkaline Leukocyte	Phosphatase Alkaline	
CCP	Lymph - Abs	Phosphatase Alkaline Liver	Phosphatase Alkaline	
	Lymph - Fra	Phosphatase Alkaline Other	Phosphatase Alkaline	
	MCH	Phosphatase Alkaline Placental	Phosphatase Alkaline	
		Platelet	Platelet	
		Potas - BSP	Serum Potassium	

About the Library

- [Main page](#)
- [Quick Look](#)
- [VAPheLib Team](#)
- [FAQ](#)

Browsing Content

- [Phenotype Catalogue](#)
- [Data Classifications](#)
- [Disease Domains](#)
- [COVID-19: Shared Data Resource](#)
- [Publications](#)

How do I contribute?

- [How to contribute](#)
- [Phenotype EntryForm](#)
- [Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

- [MVP](#)
- [CSPEAR](#)
- [VACS](#)
- [VINCI](#)
- [Other Investigators and Groups](#)

Tools

- [What links here](#)
- [Related changes](#)

Category [Discussion](#)

Category: Disease Domains

[Jump to navigation](#) [Jump to search](#)

Subcategories

This category has the following 18 subcategories, out of 18 total.

C

[Circulatory System](#)
[Congenital Anomalie](#)

D

[Dermatologic](#)
[Digestive](#)
[Disease Domains](#)

E

[Endocrine/Metabolic](#)

G

[Genitourinary](#)

H

[Hematopoietic](#)

I

[Infectious Disease](#)
[Injuries & Poisonings](#)

M

[Mental Disorders](#)
[Musculoskeletal](#)

P

[Paranoid disorders \(MAP\)](#)
[Personality disorders \(MAP\)](#)
[Pervasive developmental disorders](#)
[Phobia \(MAP\)](#)
[Polyneuropathy due to drugs \(MAP\)](#)
[Posttraumatic stress disorder \(MAP\)](#)
[Psychogenic and somatoform disorder](#)
[Psychogenic disorder \(MAP\)](#)
[Psychosis \(MAP\)](#)[PTSD \(MVP\)](#)
[PTSD Re-Experiencing \(MVP\)](#)
[PTSD \(VINCI\)](#)

R

[Risky Drinking \(VACS\)](#)

PTSD (MVP)

[Jump to navigation](#) [Jump to search](#)

Phenotype: Lifetime History of Post-Traumatic Stress Disorder (PTSD)

PhenotypeID: 00005

Status: **Validated Phenotype**

Contents

- [1 Algorithm Overview](#)
- [2 Publication](#)
- [3 Algorithm Components](#)
- [4 Validation](#)
- [5 Source of Phenotype Data](#)

Algorithm Overview

Classification: **Diseases**Related Disease Domain: **Mental Disorders**

Algorithm Description: Algorithm uses LASSO

Population: All VA users. Algorithm variation dev

Date Algorithm Created: September 14, 2016

Author: **CSP575B (MVP Alpha Project)**

Contact Rachel Quaden

Publication

Harrington K, Quaden R, et al. Validation of an Electronic Medical F

Algorithm Components

ICD-9 Codes	309.81
ICD-10 Codes	F43.10, F43.11, F43.12
Clinic Stop Codes	500-599

Validation

Algorithm Validation: Performed

Description of Validation: 500 patient charts reviewed by 5 clin

Algorithm Performance Measures: Specificity 0.98

Source of Phenotype Data

Data Sources Used:

Corporate Data Warehouse (CDW)
MVP Questionnaire Data

Role of Phenotype in Analysis: Primary Outcome / Exposure

About the Library

[Main page](#)
[Quick Look](#)
[VAPhE Lib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19: Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype Entry Form](#)
[Subscribe to the VAPhE Lib ListServ](#)

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[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)

Cooperative Studies Program Epidemiology Analytics Resource (CSPEAR)

[Jump to navigation](#) [Jump to search](#)

Contents

- 1 [Project Description](#)
- 2 [Organizational Structure](#)
 - 2.1 [Project Leadership](#)
 - 2.2 [Project Manager](#)
 - 2.3 [Lead Analyst](#)
 - 2.4 [Project Team](#)
 - 2.5 [Programmers](#)

Project Description

As part of the VA Office of Research and Development's focus on disease burden and treatment patterns, CSPEAR is a research program and anticipate future work. CSPEAR applies epidemiologic methods to analyze data. Requests from leadership and through

[Project Website](#)

Contact: CSPEAR@va.gov

[https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Cooperative_Studies_Program_Epidemiology_Analytics_Resource_\(CSPEAR\)](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/Cooperative_Studies_Program_Epidemiology_Analytics_Resource_(CSPEAR))

TBI (CSPEAR)

[Jump to navigation](#) [Jump to search](#)

Phenotype: Traumatic Brain Injury (CSPEAR)

Status: [Working Definition](#)

Contents

- 1 [Algorithm Overview](#)
- 2 [Publication](#)
- 3 [Algorithm Components](#)
- 4 [Validation](#)
- 5 [Source of Phenotype Data](#)
- 6 [Attachments](#)

Algorithm Overview

Classification: [Diseases](#)

Related Disease Domain: [Neurological](#)

Algorithm Description: TBI cases included individuals with any of the following diagnosis codes in any diagnostic position in surveillance reports. Only a single diagnosis code in any diagnostic position in primary care, mental health, polytrauma, neurology, ophthalmology, or emergency/urgent care. TBI severity classifications followed the criteria devised by the Department of Defense. TBI severity that year, regardless of diagnostic position.

Population: Veterans who received inpatient or outpatient care at a VA medical center.

Date Algorithm Created: 01/17/2020

Author: VA Cooperative Studies Program Epidemiology Analytics Resource

Contact: CSPEAR@va.gov

Publication

VA Cooperative Studies Program Epidemiology Analytics Resource

Algorithm Components

ICD-9-CM Diagnosis Codes	310.2, 800.xx, 801.xx, 803.xx, 804.xx, 850.x
ICD-10-CM Diagnosis Codes	F07.81, S02.0xxx, S02.1xxx, S02.8xxx, S02.9xxx, S07.1xxx, Z87.820
Clinic Stop Codes (any of the following stop codes in the primary position)	Primary Care: 301, 322, 323, 339, 342, 344 Mental Health: 156, 157, 501-525, 529, 530 Polytrauma: 195-198 Neurology: 315 Ophthalmology: 407 Emergency/Urgent Care: 130, 131 Other Rehabilitation: 201, 202, 204-211, 212

Validation

Algorithm Validation: Not Performed

Description of Validation: N/A

Performance Measures: N/A

Source of Phenotype Data

Data Sources Used: CDW (Corporate Data Warehouse)

Role of Phenotype in Analysis: Primary Outcome / Exposure

Attachments

Programming Code:

[TBI SQL Code](#)

[CSPEAR TBI ICD Code Set](#)

Categories: [Working Definition](#) | [Diseases](#) | [Neurological](#) | [CSPEAR](#) | [Published](#)

[Main page](#) [Discussion](#)[Read](#) [View source](#) [View history](#)

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[Jump to navigation](#) [Jump to search](#)

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[Jump to navigation](#) [Jump to search](#)

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Step 1) Fill out the [Phenotype Entry Form](#). The page will provide instructions on how to complete the form with the information on the data you would like to share with the VA Phenomics Library.

Step 2) The information on this form will not auto populate your phenotype information into the library. Your form will be reviewed by VAPheLib administrators to ensure we have all the basic information.

Step 3) VAPheLib team will work with you to finalize the information before the page is published.

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How to

Browse phenotypes: Visit the [Phenotype Catalogue](#) to search by domain or use the search function at the top of the page!

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Contact

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19:Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
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[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)

[Main page](#) [Discus](#)

VA Phen

[Jump to navigati](#)

Contents

- [1 Overview](#)
- [2 Mission](#)
- [3 Objectives](#)
- [4 How to](#)
- [5 Contact](#)

About the Library

[Main page](#)
[Quick Look](#)
[VAPheLib Team](#)
[FAQ](#)

Browsing Content

[Phenotype Catalogue](#)
[Data Classifications](#)
[Disease Domains](#)
[COVID-19:Shared Data Resource](#)
[Publications](#)

How do I contribute?

[How to contribute](#)
[Phenotype EntryForm](#)
[Subscribe to the VAPheLib ListServ](#)

Contributors and Partners

[MVP](#)
[CSPEAR](#)
[VACS](#)
[VINCI](#)
[Other Investigators and Groups](#)

Tools

[What links here](#)
[Related changes](#)
[Upload file](#)

Form:Phenotype Entry Form

[Jump to navigation](#) [Jump to search](#)

The **Phenotype Entry Form** is designed as a spring board to capture preliminary content for new users wanting to contribute phenotypes. It is designed to capture every element, but rather to serve as a basis to begin an iterative process to best showcase your work. Please enter as many fields as possible, following the conventions defined by the [VAPheLib Team](#). If you are not ready to share certain elements, please leave the fields blank, and submit as is. The information before the page is published.

If there are any questions, or you need any assistance with this form, please contact the [VAPheLib Team](#) or [Contact Us](#).

Begin by entering a phenotype in the create/edit box below.

Save your phenotype and a team member will contact you.

Please enter a short name for your phenotype using the `<PhenotypeName> [GroupName]` format. The `GroupName` in brackets is the group to which it belongs.

Overview

The VA Phenomics Development (O) Veteran Program

Mission

To provide an e

Objectives

- To provid
- To exped
- To build a

How to

[Browse phe](#)
[Contribute t](#)

Contact

YourPhenotype

Contents [hide]

- [1 Phenotype Name](#)
- [2 Classification](#)
- [3 Related Disease Domain](#)
- [4 Author](#)
- [5 Contact Email](#)

[Phenotype Name](#) [\[edit\]](#)

[Classification](#) [\[edit\]](#)

[Related Disease Domain](#) [\[edit\]](#)

[Author](#) [\[edit\]](#)

[Contact Email](#) [\[edit\]](#)

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[https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/PTSD_\(MVP\)](https://vhacdwdwhweb100.vha.med.va.gov/phenotype/index.php/PTSD_(MVP))

YourPhenotype

Contents [hide]

- 1 Phenotype Name
- 2 Classification
- 3 Related Disease Domain
- 4 Author
- 5 Contact Email

Phenotype Name [\[edit\]](#)Classification [\[edit\]](#)

Related Disease Domain

Author [\[edit\]](#)Contact Email [\[edit\]](#)

PTSD (MVP)

[Jump to navigation](#) [Jump to search](#)

Phenotype: Lifetime History of Post-Traumatic Stress Disorder

PhenotypeID: 00005

Status: **Validated Phenotype**

Contents

- 1 [Algorithm Overview](#)
- 2 [Publication](#)
- 3 [Algorithm Components](#)
- 4 [Validation](#)
- 5 [Source of Phenotype Data](#)

Algorithm Overview

Classification: [Diseases](#)

Related Disease Domain: [Mental Disorders](#)

Algorithm Description: Algorithm uses LASSO modeling to

Population: All VA users. Algorithm variation developed for u

Date Algorithm Created: September 14, 2016

Author: [CSP575B \(MVP Alpha Project\)](#)

Contact: Rachel Quaden

Publication

Harrington K, Quaden R, et al. Validation of an Electronic Medical Record-Based Algorithm for Identifying Posttr

Algorithm Components

ICD-9 Codes	309.81
ICD-10 Codes	F43.10, F43.11, F43.12
Clinic Stop Codes	500-599

Validation

Algorithm Validation: Performed

Description of Validation: 500 patient charts reviewed by 5 clinicians. 25% of charts reviewed by 2 reviewers.

Algorithm Performance Measures: Specificity 0.98

Source of Phenotype Data

Data Sources Used:

- Corporate Data Warehouse (CDW)
- MVP Questionnaire Data

Role of Phenotype in Analysis: Primary Outcome / Exposure

Categories: [Diseases](#) | [Mental Disorders](#) | [CSP575B](#) | [PhenotypeID Assigned](#) | [Validated Phenotype](#) | [Publis](#)