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
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

❖ 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 Schehnet, 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

THANK YOU!
VA’s **Phenomenal Pheno**mics Library Team

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

| MVP001: Peter Wilson, Kelly Cho | MVP004: Amy Justice, Henry Kranzler |
| MVP003/MVP028: Phillip Tsao, Kyong-Mi | MVP006: Panagiotis Roussos |
| MVP005/MVP24: Neal Peachy | MVP008: Shiuw-Wen, Cynthia Brandt, Sally Haskell |
| MVP007: Marcos Bamman | MVP010: Alan Ryan |
| MVP009: Lawrence Phillips | MVP011: Jean Beckham, Nathan Kimbrel, Phillip Harvey, David Oslin, Benjamin McMahon |
| MVP012: Kyle Kampman | MVP013: Steven Zelidat |
| MVP014: Scott Damrauer, Christopher O’Donnell, Phillip Tsao, Ravi Madduri | MVP015: Mark Logue |
| MVP016: Jennifer Lee, Tim Assimes |
| MVP017: Amy Justice, Michael Gaziano, Francis Alexander | MVP018: Jennifer Lee |
| MVP019: James Ashe |
| MVP020: Donna White | MVP021: Edward Siew, Michael Matheny |
| MVP022: Richard Hauger | MVP023: Fatemeh Hahgighi |
| MVP026: Victoria Merritt | MVP029: Dawn Proenzale, Drew Helmer |
| MVP030: Jason Vassy | MVP031: Bruce Montgomery |
| MVP032: Reid Thompson | MVP033: Marianna Gasperi |
| MVP034: Shaija Shah | BDS001: Nikhil Munshi, Saiju Pyarajan |
| BDS002: Saiju Pyarajan |

- **MVP-VAPheLib is managed and maintained by MVP Data Core:** [MVPDataCore@va.gov](mailto:MVPDataCore@va.gov)
  (Lauren Costa, Anne Ho, Petra Schubert, Laura Tarko, Nicholas Link, Katherine Liao, Tianxi Cai, Mai Nguyen, Rebecca Song, Hanna Gerlovin)

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**THANK YOU!**

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

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@VAWW.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**

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**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

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Findable/Accessible/Interoperable/Reusable

**VAPheLib – In Perspective**

- **1997**: Boston CSP Epi Center launched
- **2010**: MVP launched
- **5/30/2017**: MVP ~570K, 8 Projects
- **12/10/2019**: MVP ~810K, 35 Projects
- **4/6/2020**: Kick-off meeting for VA-wide expansion, VAPheLib project plan developed
- **5/12/2020**: Library opened to VA-wide, in support of VA COVID-19 Shared Data Resources

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**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)

**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

**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

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**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.

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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:

  Myocardial infarction (MI)

  1 inpatient ICD code (410-411) for ischemic heart disease
  or
  2 outpatient ICD codes (410-411) for ischemic heart disease

• 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
# VAPheLib Project Plan

## IV. Project Management Plan
### A. Project Timeline - Tentative

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

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

Number of Unique Users

May 7, 2020
N=741

April 6, 2020
VAPheLib – Utilization By Station

Top 10 VA Sites
- Boston
- Salt Lake City
- Seattle
- Washington
- Palo Alto
- West Haven
- Durham
- Hines
- Bronx
- Miami
# VA PheLib – Phenomics Data Coverage

<table>
<thead>
<tr>
<th>Data Classifications</th>
<th>Total Phenotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Demographics</td>
<td>7</td>
</tr>
<tr>
<td>Vitals</td>
<td>6</td>
</tr>
<tr>
<td>Laboratory</td>
<td>77</td>
</tr>
<tr>
<td>Medications</td>
<td>52</td>
</tr>
<tr>
<td>Procedures</td>
<td>7</td>
</tr>
<tr>
<td>Diseases</td>
<td>1,991*</td>
</tr>
<tr>
<td>Lifestyle &amp; Environmental Factors</td>
<td>16</td>
</tr>
<tr>
<td>Total</td>
<td>2,156**</td>
</tr>
</tbody>
</table>


(Data as of May 8, 2020)

<table>
<thead>
<tr>
<th>Curation Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>In Progress</td>
</tr>
<tr>
<td>Working Definition</td>
</tr>
<tr>
<td>Validated Phenotype</td>
</tr>
</tbody>
</table>

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

✓ Become a Contributor! Become a Partner!
  o Join our partners group by contributing and sharing your expertise with VA community
  o 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!
  o 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

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://vhacdwwhweb100.vha.med.va.gov/phenotype/index.php/VA_Phenomics_Library

- Examples of phenotype metadata

- How to contribute
VA Phenomics Library

Overview

The VA Phenomics Library (VAPheLib) is a shared knowledgebase of VA EHR-based phenotype definitions developed by the Office of Research Development (ORD). This effort is part of an enterprise-wide approach to promote a resource through the VA Veteran Program (MVP), Cooperative Studies Program (CSP), and VA Informatics and Computing Institute (VACI).

Mission

To provide an encyclopedia of VHA EMR-based phenotyping through integration of phenome and clinical knowledge.

Objectives

1. To provide a knowledgebase framework to collect, store/archive and share phenotype definitions.
2. To expedite VA science by enabling phenotype reusability and scalability across VA programs.
3. To build a platform to encourage and enhance collaboration and communication across VA.

How to

Browse phenotypes: Visit the Phenotype Catalogue to search by domain or use the search tool.
Contribute to the Library: Visit the How to contribute page to find how to showcase your work.

Contact
VA Phenomics Library

Overview

The VA Phenomics Library (VAPhLib) is a shared knowledgebase of VHA EHR-based phenotypes, designed under the Office of Research and Development (ORD). This effort is part of an enterprise-wide approach to provide a resource for Veteran Program (MVP), Cooperative Studies Program (CSP), and VA Informatics and Computing (VIC). The library serves as a central location for contributing, sharing, and browsing content curated by VA researchers and clinical stakeholders.

Mission

To provide an encyclopedia of VHA EHR-based phenotyping through integration of phenomics and genomics.

Objectives

1. To provide a knowledgebase framework to collect, store, archive and share phenotype definitions.
2. To expedite VA science by enabling phenotype reusability and scalability across VA projects.
3. To build a platform to encourage and enhance collaboration and communication across the VA Research Enterprise.

How to

Browse phenotypes: Visit the Phenotype Catalogue to search by domain or use the search bar.
Contribute to the Library: Visit the How to Contribute page to find how to showcase your work.

Contact
VA Phenomics Library

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) of the Department of Veterans Affairs (VA), Cooperative Studies Program (CSP), and Vanderbilt University (VU).

Contributors and Partners

The content of this knowledgebase is a collective work across many VA research groups and investigators. We truly appreciate their valuable contributions. Contributors 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 contact us at VA@healthdata.org 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
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: VU (Scott DuVall, Ph.D, Kevin Malhoti, BS and Tori Anglin-Foote, MHA)

Contact us at VAPheLib@va.gov
Frequently Asked Questions

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Contents

1. How do I navigate the VA Phenomics Library?
2. How do I contribute content to the library?
3. How do I search phenotypes? Are all the phenotypes available in the VA Phenomics Library Validated?
4. How do I use the information available in the library for my own study?
5. What should I do if I need data that is not already provided for my study?
6. Information regarding the Million Veteran Program (MVP), does this mean I can use MVP data for my study?
7. 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 the 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 evaluate if the phenotype is validated. Additionally, each phenotype within the VAPheLib is categorized by status (In Progress, Working Definition, and Valid) when navigating 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?


Phenotype Overview

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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
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
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 a total of 3723 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 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 nervous system (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 gut (MAP)
Abnormality of organs and soft tissues of pelvic (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 extrahepatic bile ducts (MAP)
Malignant neoplasm of kidney, except nephroblastoma (MAP)
Malignant neoplasm of liver, primary (MAP)
Malignant neoplasm of other and ill-defined sites of alimentary tract (MAP)
Malignant neoplasm of other urinary system (MAP)
Malignant neoplasm of ovary and other female reproductive organs (MAP)
Malignant neoplasm of ovary (MAP)
Malignant neoplasm of rectum, rectosigmoid (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 site (MAP)
Malignant neoplasm of uterus (MAP)
Malignant neoplasm, other (MAP)
Malignant neoplasm, peripheral (MAP)
Malposition and malpresentation of fetus (MAP)
Malunion and nonunion of fracture (MAP)
Mammographic microcalcification (MAP)
Mammary and unknown neoplasms of female breast (MAP)
Mastodynia (MAP)

N

Nood disorders (MAP)
Nordic obesity (MAP)
Noyamoya disease (MAP)
MRSA pneumonia (MAP)
Mucus polyt of cervix (MAP)
Multiple gestation (MAP)
Multiple Myeloma (MAP)
Multiple myeloma (MAP)
Multiple sclerosis (MAP)
Muscle-limb-speech (MAP)
Muscle weakness (MAP)
Muscular atrophy and disuse atrophy (MAP)
Musculoskeletal symptoms referable to limbs (MAP)
Nyalgia and myositis unspecified (MAP)
Myasthenia gravis (MAP)
Mycoes (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)
Myocardiitis (MAP)
Myodystrophy (MAP)
Myoneural disorders (MAP)
Myopathy (MAP)
Myopia (MAP)
Myringitis (MAP)
Myocardial Infarction MI (SAFE)

Algorithm Overview

Classification: Diseases

Related Disease Domain: Circulatory System

Algorithm Description: The SAFE method uses structured data filtering for patients with a Myocardial Infarction (MI). If a patient only had an MI and had at least two notes in the CDW data, then they met the filter criteria.

1. Application of broad ICD code filter to identify possible MI patients with at least two notes in the CDW data.
2. Select features for model training including relevant features only used for the filter. Create MI dictionary by major criteria.
3. Model training with gold standard labels.

Final model (after orthogonalizing the features): logit Pr(MI) = 0.5419398 * log(1 + C002962) - 0.6731429 * log(1 + Noise) + Constant

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 0.842.

Assuming that the filter negative patients don’t have MI, the model achieves

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 Assignment

Phenotype Table

Value: Yes, No

"Yes": Value_Probability >= 0.758 (Patient has MI)
"No": Value_Probability < 0.758

Value_Probability: 0-1

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

Myocardial infarction/Coronary Artery Disease (VACS)
410.x, 411.x, 412, 413, 429.7, V45.81, V45.82
2 KB (225 words) - 13:41, 6 December 2019

Cardiovascular Disease (VNCI)
OR ICD9 code '411'
4 KB (621 words) - 14:15, 10 March 2020

Primary biliary cirrhosis (MAP)
411
4 KB (591 words) - 14:15, 6 February 2020

Unstable angina (Intermediate coronary syndrome) (MAP)
4 KB (528 words) - 14:15, 6 February 2020

Coronary atherosclerosis (MAP)
|Phe411.4 (411.81, 414.00, 414.05, 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, 410.51, 410.92, 411.0, 412_, 429.7, 429.71, 429.79 (ICD9):23.6, 23.3, 21, 25.2, 25.3, 222.
5 KB (534 words) - 13:05, 11 February 2020

Map usp Conditions
,(4,1,ICD,'411.1'),(4,2,ICD,'411.1')
191 KB (20,970 words) - 11:41, 22 September 2017
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)
- Antilipids (Class)
- Anticoagulants (Class)
- Antihypertensive Combinations (Class)
- Antihypertensive Medications (Nashville)
- Antihypertensives, other (Class)
- Antilipemic Agents (Class)
- Aspirin
- Asthma Medications

B
- Beta Blockers (Class)

C
- Cabazitaxel (VNCI)
- Calcium Channel Blockers (Class)
- Carbonic Anhydrase Inhibitor Diuretics (Class)
- Chemotherapy Medications (VNCI)
- COPD Medications

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Browsing Tips
- Medication data used for various projects/cohorts and purposes

- Heart Failure Medications
- Hepatitis C Medications
- Highest Morphine Equivalent Daily Dose (MEDD) for chronic pain treatment
- HIV Medications
- Hypoglycemic Agents, Other (Class)
- Hypothyroid Medications (VNCI)
- Insulin (Class)
- Insulin Medication (VNCI)
- Leuprolide (VNCI)
- Loop Diuretics (Class)
- MEED Phenotypes
- Medication Persistence (VACS)
- Medications SOP, VNCI
- Mental Health Medications
- Morphine Equivalent Daily Dose (MEDD) during inpatient stay hip and knee arthroplasty
- Oral Hypoglycemic Agents (Class)
- Palliative (Velasco) Medication (VNCI)
- Peripheral Vasodilators (Class)
- Platelet Aggregation Inhibitors (Class)
- Potassium Sparing/Combination Diuretics (Class)
- Psychiatric Medications (VNCI)
- Pulmonary Fibrotic Disease Medications
Anti-hypertensive Medications (Nashville)

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 ('HYDRAZINE', 'METHYLOPA', 'CLONIDINE') THEN 'VASODILATOR'
END AS DRUG_CLASS_3
FROM

( select LocalDrugSID,
    LocalDrugNameWithDose,
    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 CDWWork.dim.LocalDrug
where drugclass = 'CV400'
and len(DrugNameWithoutDose) = len(replace(DrugNameWithoutDose, '/', '')) = 1
union
select
  LocalDrugSID,
  LocalDrugNameWithDose,
  DrugClass,
  substring(DrugNameWithoutDose, 1, (charindex('/', DrugNameWithoutDose, 1)-1)) combo_drug_1,
  substring(DrugNameWithoutDose, 1, (charindex('/', DrugNameWithoutDose, 1)-1)) combo_drug_2,
  reverse(substring(reverse(DrugNameWithoutDose), 1, (charindex('/', reverse(DrugNameWithoutDose), 1)-1))) combo_drug_3
  from CDWWork.dim.LocalDrug
where drugclass = 'CV400'
and len(DrugNameWithoutDose) = 1
)
, tab_columns AS
( select
  LocalDrugSID,
  localdrugnamewithoutdose,
  DRUGCLASS,
  DRUG_CLASS_1,
  DRUG_CLASS_2,
  DRUG_CLASS_3
  from HYPERTENSION_COMBO_MEDS)

select
LocalDrugSID,
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<tr>
<th>Labs Adjudicated</th>
<th>Calcium - BSP</th>
<th>C-peptide</th>
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<tr>
<td>Shortname</td>
<td>CCP</td>
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<tr>
<td>A1C</td>
<td>Chloride - BSP</td>
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</tr>
<tr>
<td>ABO Type</td>
<td>CKMB - Abs</td>
<td></td>
</tr>
<tr>
<td>Albumin</td>
<td>CKMB - Fra</td>
<td></td>
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<tr>
<td>ALT</td>
<td>Creat - BSP</td>
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<tr>
<td>AST</td>
<td>CRP</td>
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<tr>
<td>Baso - Abs</td>
<td>eGFR</td>
<td></td>
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<tr>
<td>Baso - Fra</td>
<td>Eos - Abs</td>
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<td>Bicarbonate</td>
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<td>Bilirubin indirect</td>
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<td>Bilirubin Stick</td>
<td>HCV - RNA VL</td>
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<td>Bilirubin Total</td>
<td>HCV - bDNA VL</td>
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<tr>
<td>Bilirubin Total and Direct</td>
<td>HCV - Genotype</td>
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<td>Bilirubin Unconjugated</td>
<td>HDLC</td>
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<td>BUN - BSP</td>
<td>LDLc</td>
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<td>Calcium - BSP</td>
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</tr>
<tr>
<td>C-peptide</td>
<td>Lymph - Fra</td>
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<tr>
<td>Creatine Kinase (VNIc)</td>
<td>MCH</td>
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<tr>
<td>CRP</td>
<td>MCHC</td>
<td>Mean Corpuscular Hemoglobin Concentration (MCHC)</td>
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<td>MCV</td>
<td>Mean Corpuscular Volume (MCV)</td>
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<td>Mg - BSP</td>
<td>Serum Magnesium</td>
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<td>Mono - Fra</td>
<td>Monocyte - Fractional Value</td>
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<td>Mean Platelet Volume (MPV)</td>
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<td>Neutrophil - Absolute Value</td>
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<tr>
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<td>Neut - Fra</td>
<td>Neutrophil - Fractional Value</td>
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<td>Phosphatase Alkaline</td>
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<td>Phosphatase Alkaline (Specialty L)</td>
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<td>Phosphatase Alkaline Bone</td>
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<td>Phosphatase Alkaline Heat Stable</td>
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<td>Phosphatase Alkaline Intensive</td>
<td>Phosphatase Alkaline</td>
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<td>Phosphatase Alkaline isoenz</td>
<td>Phosphatase Alkaline</td>
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<td>Phosphatase Alkaline Leukocyte</td>
<td>Phosphatase Alkaline</td>
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<td>Phosphatase Alkaline Liver</td>
<td>Phosphatase Alkaline</td>
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<tr>
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<td>Phosphatase Alkaline Other</td>
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<td>Platelet</td>
<td>Platelet</td>
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<td></td>
<td>Potas - BSP</td>
<td>Serum Potassium</td>
</tr>
</tbody>
</table>
Cooperative Studies Program Epidemiology Analytics Resource (CSPEAR)

TBI (CSPEAR)

Algorithm Overview

Classification: Diseases
Related Disease Domain: Neurological

Algorithm Description: TBI cases included individuals with any of the following ICD-9-CM Diagnosis Codes:
- Primary Care: 310.2, 800.xx, 801.xx, 803.xx, 804.xx, 805.xx
- Mental Health: F07.81, S02.8xx, S02.1xx, S02.8xx, S02.9xx
- Polytrauma: S07.1xx, Z87.820
- Clinic Stop Codes (any of the following stop codes in the primary position)
- Emergency/Urgent Care: 130, 131
- Other Rehabilitation: 201, 202, 204-211, 2

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
- CSPPEAR TBI ICD Code Set

Categories: Working Definition, Diseases, Neurological, CSPPEAR, Published
How to contribute

It’s easy to begin a page with your data element/phenotype. VAPheLib Team will work with you to finalize your page before it is populated and shared.

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.

Should you have any questions about your submission in the meantime, please contact VAPheLib@va.gov.

How to

Browse phenotypes: Visit the Phenotype Catalogue to search by domain or use the search function at the top of the page.

Contribute to the Library: Visit the How to contribute page to find how to showcase your work!

Contact
Form: Phenotype Entry Form

The Phenotype Entry Form is designed as a spring board to capture preliminary content for new users wanting to contribute phenotypes. It allows you 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 you can. Be sure to follow the conventions defined by the VA Phenotype Library. If you are not ready to share certain elements, please leave the fields blank, and submit as is. We may contact you after your submission to give you feedback on your submission.

If there are any questions, or you need any assistance with the form, please contact VA Phenotype Library.

Overview

The VA Phenotype Library

Mission

To provide an entry to contribute new phenotypes.

Objectives

1. To provide a new means for contribution.
2. To expedite the entry process for contributors.
3. To build a collaborative library.

How to

Browse phenotypes

Contribute new phenotypes

Contact

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 VA Phenotype Library

Contributors and Partners

VA

CSPAR

VACS

VINCI

Other Investigators and Groups

Tools

What links here

Related changes

Upload file

Your Phenotype

Phenotype Name

Classification

Related Disease Domain

Author

Contact Email
PTSD (MVP)

Phenotype: Lifetime History of Post-Traumatic Stress Disorder

PhenotypeID: 00005

Status: Validated Phenotype

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

Algorithm Components

<table>
<thead>
<tr>
<th>ICD-9 Codes</th>
<th>309.81</th>
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<tbody>
<tr>
<td>ICD-10 Codes</td>
<td>F43.10, F43.11, F43.12</td>
</tr>
<tr>
<td>Clinic Stop Codes</td>
<td>500-599</td>
</tr>
</tbody>
</table>

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, Publish