Conflict of interest statement

David S. Carrell receives research funding from the U.S. Food and Drug Administration (FDA) to develop methods to improve capacity for conducting medical product safety studies using electronic health record (EHR) data and computable phenotyping algorithms. He has no other conflicts of interest to report.

Scalable Algorithm Development: An Alternative to Algorithm Reuse?

David S. Carrell, PhD
Associate Investigator
Kaiser Permanente Washington Health Research Institute
Seattle, WA

For presentation at the 2022 ISPOR meetings, May 17, 2022

Disclaimer

The views expressed in this presentation represent those of the presenters and do not necessarily represent the official views of the U.S. FDA.

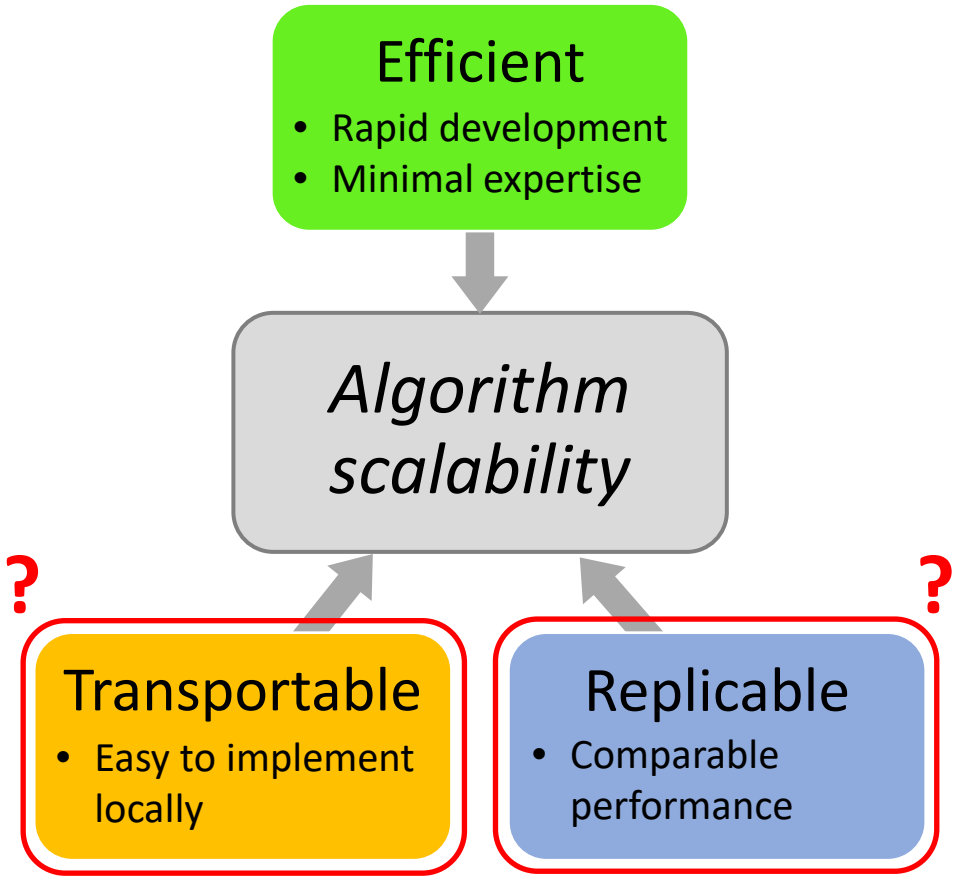
Overview

- *The appeal (and challenges) of algorithm reuse*
- *Is scalable algorithm development an alternative to reuse?*
- *Example: Automated development of a COVID-19 algorithm*

Why is algorithm reuse appealing?

Saves time and money! **Reusing algorithms avoids …**

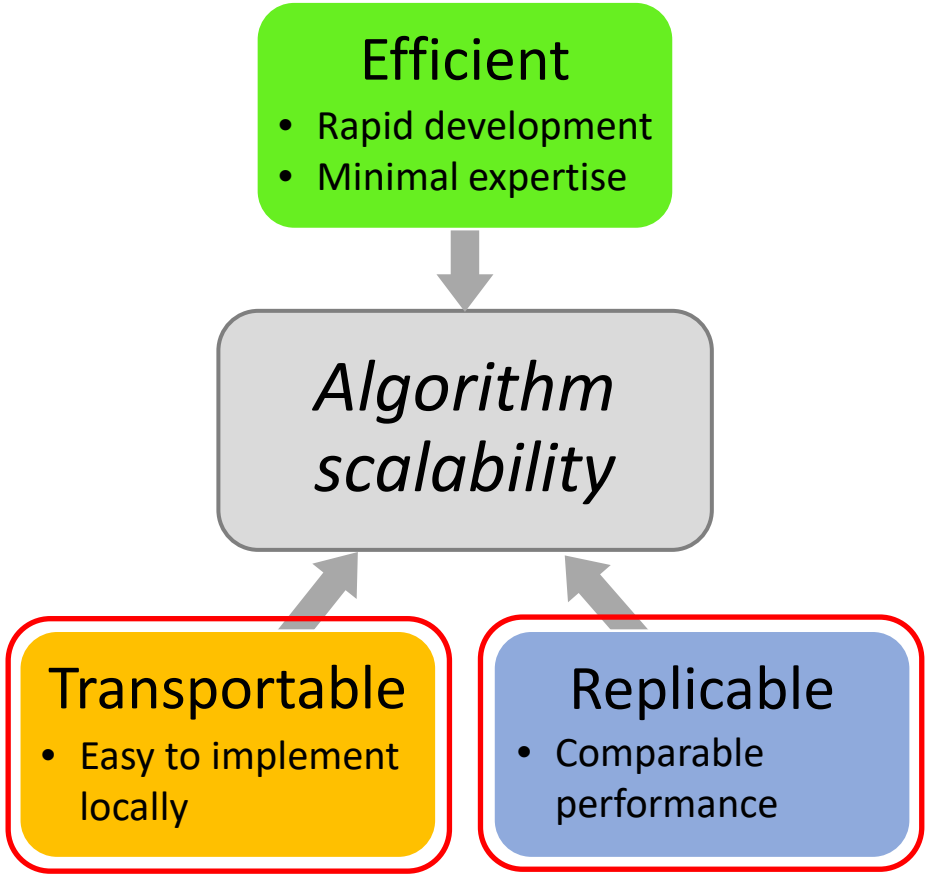
- *Algorithm design costs*
  - Statistical, clinical, informatics expertise
- *Gold standard creation costs (some)*
  - Clinical expertise
  - Time-intensive
- *Feature engineering costs*
  - Clinical, informatics EHR/NLP expertise
  - Time-intensive
- *Model training/evaluation costs*
  - Statistical expertise



Why is algorithm reuse challenging?

It's hard!

- Transporting algorithms requires …
  - *Translation to local data*
  - *Modification for missing/different data*
  - *Using unfamiliar code/software*
- Replication challenges …
  - *Different patient populations*
  - *Different care settings, specialties*
  - *Different data capture*
  - *Different coding practices, terminology*
  - *Different predictor-outcome relationships*



Is there another path to *algorithm scalability?*

What if algorithm development costs were reduced so much it was feasible to *implement the entire development process in each setting*?

This is the goal of automated phenotyping methods [1-5]

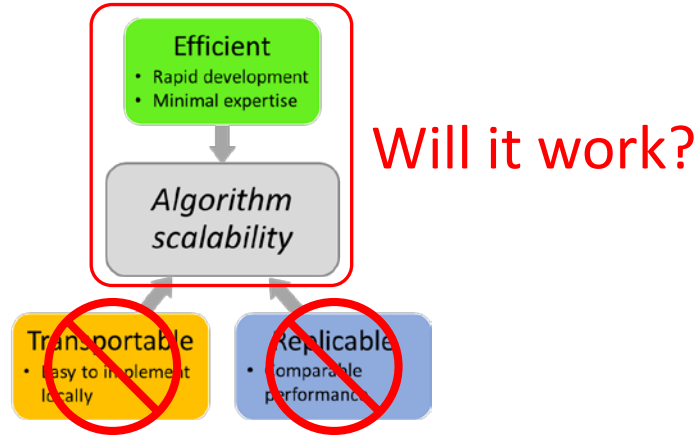
- Automate *NLP dictionary* creation (mine terms from clinical articles [1])
- Apply NLP to patient notes to create *simple NLP features* [1-5]
  - (Automation of dx features also possible [5])
- Use *silver labels* (e.g., diagnosis counts) to train models [2-5]
- Use *machine learning* methods to train models [2-5]

Implementation time measured in *days* (not months)

1. **Yu** et al. Toward high-throughput phenotyping: unbiased automated feature extraction and selection from knowledge sources. JAMIA 2015
2. **Yu** et al. Surrogate-assisted feature extraction for high-throughput phenotyping. JAMIA 2017
3. **Yu** et al. Enabling phenotypic big data with PheNorm. JAMIA 2018
4. **Zhang** et al. High-throughput phenotyping with EMR data using a common semi-supervised approach (PheCAP). Nature Protocols. 2019
5. **Liao** et al. High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. JAMIA 2019

Example: Automated COVID-19 phenotyping

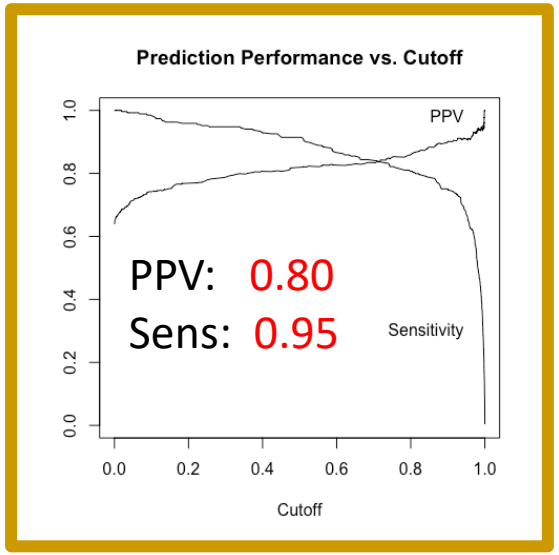
Implement *from scratch at* VUMC and *at* KPWA an automated phenotyping method (*PheNorm*[3])



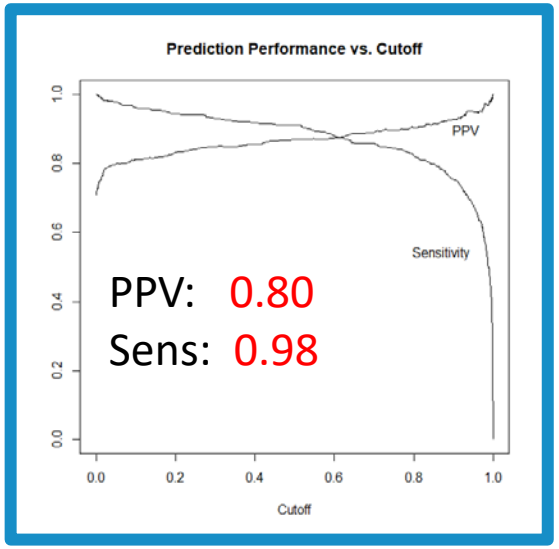
Will it work?

- **Potential cases**: Patients with ≥1 COVID-19-related dx
  - *VUMC: 24,355*
  - *KPWA: 8,329*
- **NLP dictionary**: 166 terms from "COVID-19" clinical knowledge sources
- **Apply NLP** to notes +/-30 days of the COVID-19 dx
- **Machine learned model** to predict true cases
  - **Silver label**: Counts of COVID-19 dxs, mentions
  - **R code**: https://github.com/celehs/PheNorm
- **Evaluate** in gold-labeled random sample (~60% true case rate)

Vanderbilt University Medical Center (~inpatient)



Kaiser Permanente Washington (~outpatient)



3. **Yu** et al. Enabling phenotypic big data with PheNorm. JAMIA 2018.

Contact information

David S. Carrell, PhD

david.s.carrell@kp.org

Kaiser Permanente Washington Health Research Institute

Seattle, WA, USA