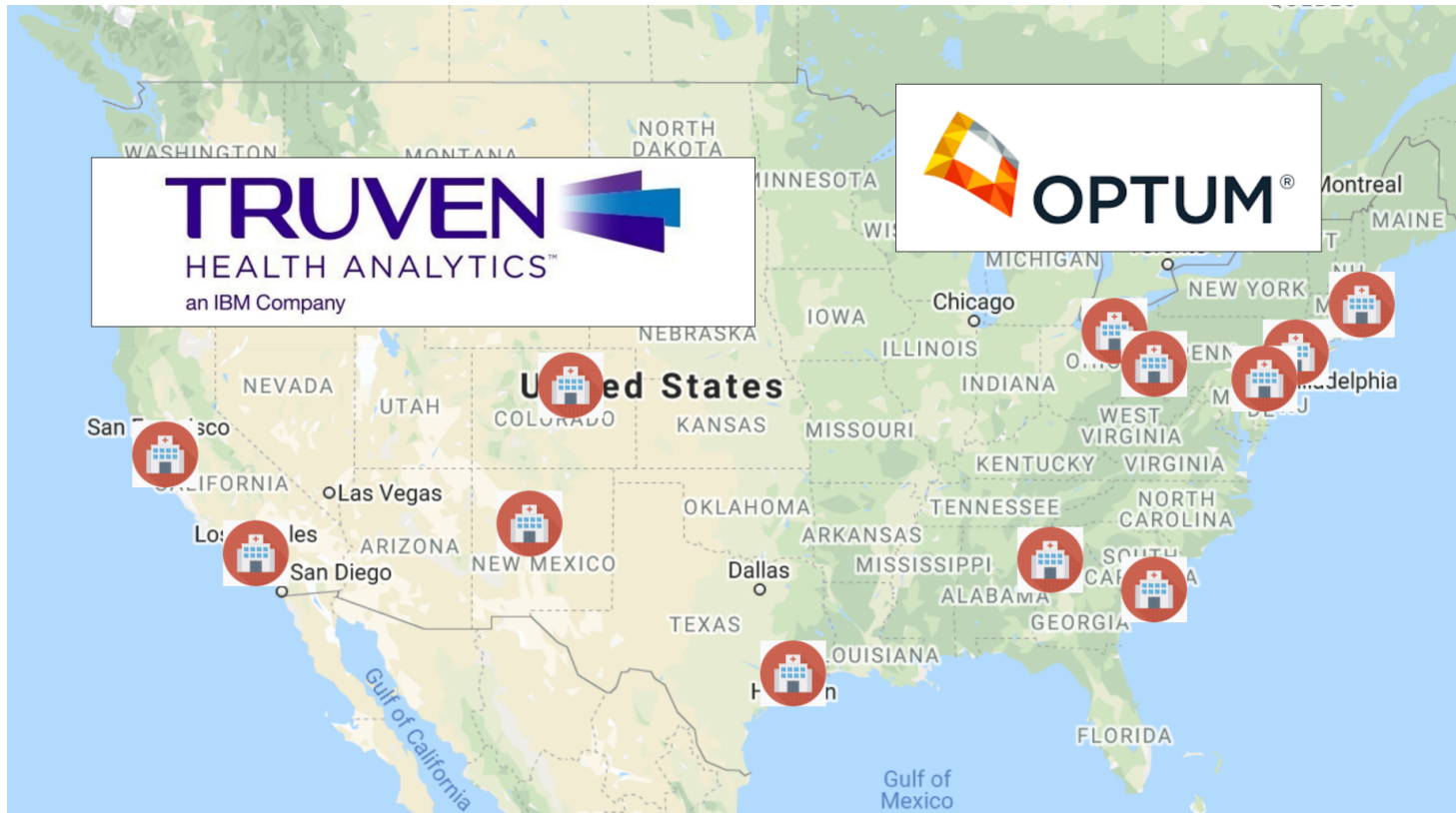


# Large-scale Bayesian sparse regression for OHDSI network studies

Aki Nishimura

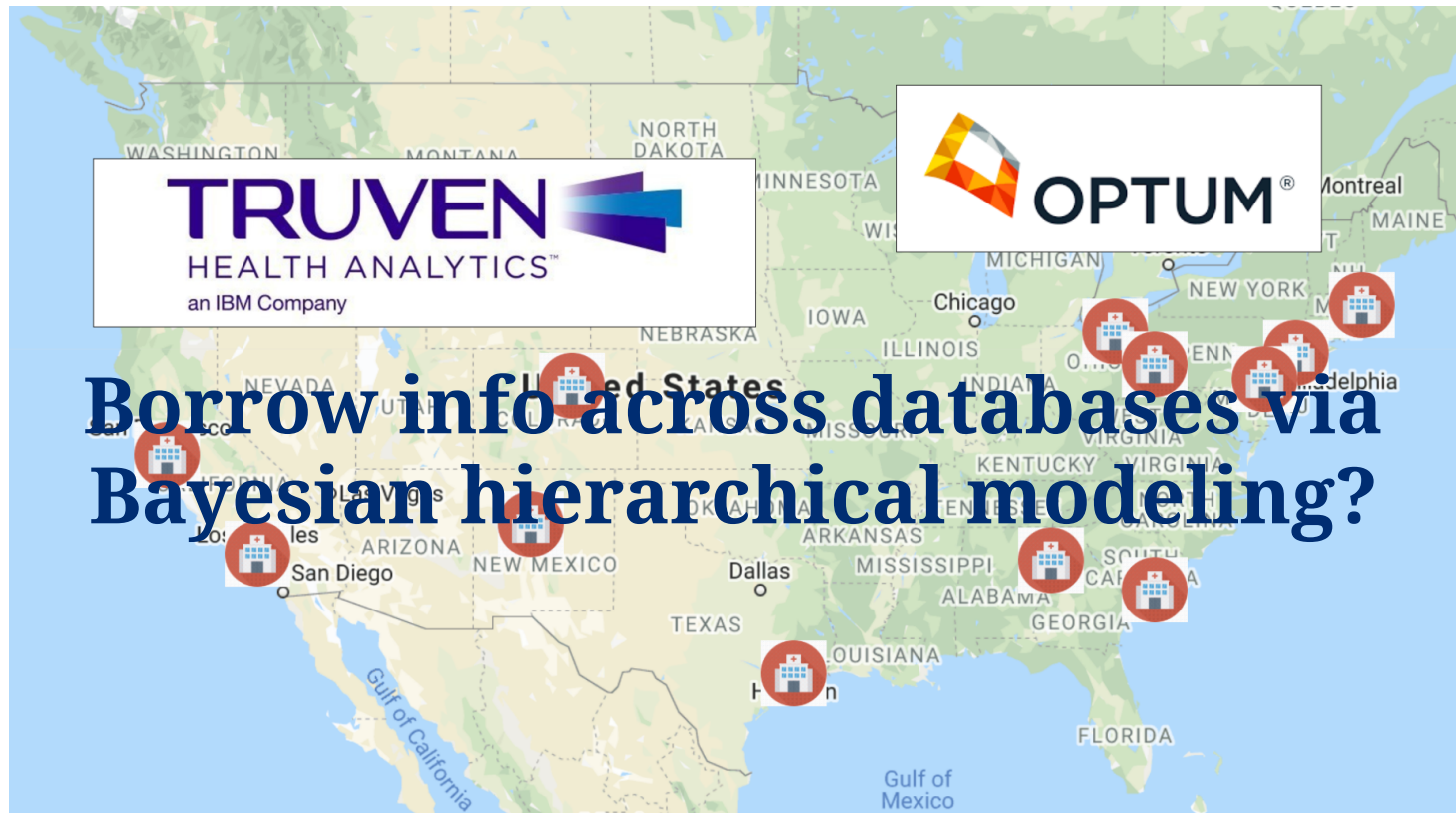
# ~~Problem~~ Opportunity for OHDSI

Many health databases are too small & too heterogeneous.



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# Large-scale $L^1$ -penalized regression: a statistical engine behind OHDSI studies

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International Journal of  
**Epidemiology**



## Evaluating large-scale propensity score performance through real-world and synthetic data experiments FREE

Yuxi Tian ✉, Martijn J Schuemie, Marc A Suchard

*International Journal of Epidemiology*, Volume 47, Issue 6, December 2018, Pages 2005–2014,  
<https://doi.org/10.1093/ije/dyy120>

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# Large-scale $L^1$ -penalized regression: a statistical engine behind OHDSI studies

## Cyclops

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 R-CMD-check  passing  codecov  67%  CRAN  3.1.2  downloads  933/month

Cyclops is part of the [HADES](#).

## Introduction

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Cyclops (Cyclic coordinate descent for logistic, Poisson and survival analysis) is an R package for performing large scale regularized regressions.

## Examples

---

```
library(Cyclops)
cyclopsData <- createCyclopsDataFrame(formula)
cyclopsFit <- fitCyclopsModel(cyclopsData)
```

# Penalized vs. Bayesian sparse regression

Under Bayes, data  $\mathbf{y}$  and  $\mathbf{X}$  inform unknown  $\beta$  via:

$$\pi_{\text{post}}(\beta \mid \mathbf{y}, \mathbf{X}) \propto L(\mathbf{y} \mid \mathbf{X}, \beta) \pi_{\text{prior}}(\beta).$$

# Penalized vs. Bayesian sparse regression

Using prior is analogous to placing *penalty* on  $\beta$ :

$$\hat{\beta} = \operatorname{argmin}_{\beta} \{-\log L(\mathbf{y} \mid \mathbf{X}, \beta) + \operatorname{pen}(\beta)\}$$

where  $\operatorname{pen}(\beta)$  “=”  $-\log \pi_{\text{prior}}(\beta)$ .

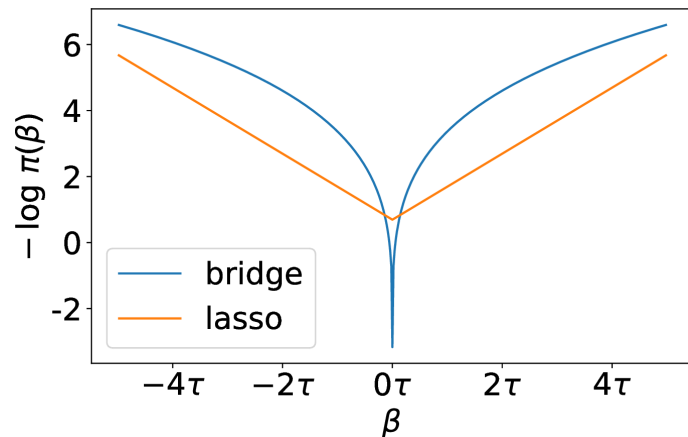
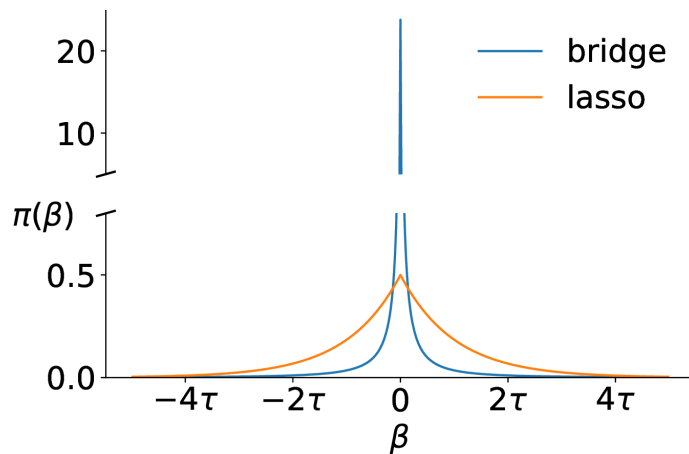


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where  $\operatorname{pen}(\beta)$  “=”  $-\log \pi_{\text{prior}}(\beta)$ .



**Example:** Bridge prior  $\pi_{\text{prior}}(\beta_j \mid \tau) \propto \tau^{-1} \exp(-|\beta_j/\tau|^\alpha)$

# "Bayes doesn't scale"?

Bayesians often rely on *Monte Carlo* simulation, drawing

$$\boldsymbol{\beta}^{(1)}, \dots, \boldsymbol{\beta}^{(M)} \sim \pi_{\text{post}}(\cdot \mid \mathbf{y}, \mathbf{X}),$$

and use  $M^{-1} \sum_m \delta_{\boldsymbol{\beta}^{(m)}}(\cdot)$  to quantify the posterior.

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This computation can be **prohibitively expensive**.

# "Bayes doesn't scale"



Theory and Methods

## Prior-Preconditioned Conjugate Gradient Method for Accelerated Gibbs Sampling in “Large $n$ , Large $p$ ” Bayesian Sparse Regression

Akihiko Nishimura   & Marc A. Suchard 

Received 11 Feb 2020, Accepted 18 Mar 2022, Accepted author version posted online: 27 Mar 2022, Published online: 09 May 2022

 Download citation  <https://doi.org/10.1080/01621459.2022.2057859>



# ~~"Bayes doesn't scale"~~

**Example:** Compare alt. treatments for atrial-fibrillation, blood anti-coagulants *dabigatran* and *warfarin*.

**Objective:** Study relative risk of *gastrointestinal bleeding*.

- $n = 72,489$  patients, 27.3% dabigatran users
- $p = 22,175$  covariates

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**Objective:** Study relative risk of *gastrointestinal bleeding*.

- $n = 72,489$  patients, 27.3% dabigatran users
- $p = 22,175$  covariates

**Computing time:** With the **previous state-of-the-art**,

- Propensity score model
  - **106** hours for 5,500 iterations,
- Outcome model with subgroup-effect interactions
  - **212** hours for 11,000 iterations.

# ~~"Bayes doesn't scale"~~

**Example:** Compare alt. treatments for atrial-fibrillation, blood anti-coagulants *dabigatran* and *warfarin*.

**Objective:** Study relative risk of *gastrointestinal bleeding*.

- $n = 72,489$  patients, 27.3% dabigatran users
- $p = 22,175$  covariates

**Computing time:** With the new algorithm,

- Propensity score model
  - 11.4 hours (9.3-fold speedup) for 5,500 iterations,
- Outcome model with subgroup-effect interactions
  - 11.3 hours (18.8-fold speedup) for 11,000 iterations.

# ~~"Bayes doesn't scale"~~

**Example:** Compare alt. treatments for atrial-fibrillation, blood anti-coagulants *dabigatran* and *warfarin*.

**Objective:** Study relative risk of *gastrointestinal bleeding*.

- $n = 72,489$  patients, 27.3% dabigatran users
- $p = 22,175$  covariates

**Computing time:** With the new algorithm + GPU,

- Propensity score model
  - 0.62 hours (171-fold speedup) for 5,500 iterations,
- Outcome model with subgroup-effect interactions
  - 0.61 hours (347-fold speedup) for 11,000 iterations.



# New algorithm in Python's BayesBridge



## BayesBridge

Python package for Bayesian sparse regression, implementing the standard (Polya-Gamma augmented) Gibbs sampler as well as the CG-accelerated sampler of Nishimura and Suchard (2018). The latter algorithm can be orders of magnitudes faster for a large and sparse design matrix.

## Installation

```
pip install bayesbridge
```

## Background

The Bayesian bridge is based on the following prior on the regression coefficients  $\beta_j$ 's:

$$\pi(\beta_j | \tau) \propto \tau^{-1} \exp(-|\beta_j|/\tau^\alpha) \text{ for } 0 < \alpha \leq 1$$

The Bayesian bridge recovers the the Bayesian lasso when  $\alpha = 1$  but can provide an improved separation of the significant coefficients from the rest when  $\alpha < 1$ .

## Usage

```
from bayesbridge import BayesBridge, RegressionModel, RegressionCoefPrior

model = RegressionModel(y, X, family='logit')
prior = RegressionCoefPrior(bridge_exponent=.5)
bridge = BayesBridge(model, prior)
mcmc_output = bridge.gibbs(
    n_burnin=100, n_post_burnin=1000, thin=1,
    coef_sampler_type='cholesky' # Try 'cg' for large and sparse X
)
coef_samples = mcmc_output['samples']['coef']
```

# bayesbridger: R wrapper based on reticulate

Set up Python environments,

```
library(bayesbridger)
configure_python(envname = "bayesbridge")
```

instantiate BayesBridge with data  $y$  and  $X$ ,

```
model <- create_model(y, X)
prior <- create_prior(bridge_exponent=.25)
bridge <- instantiate_bayesbridge(model, prior)
```

and sample from the posterior!

```
gibbs_output <- gibbs(bridge, n_iter = 1000L,
                      coef_sampler_type = "cg")
mcmc_samples <- gibbs_output$samples
```

Thank you!