

Breast Cancer Diagnosis

Wenhan Bao | Tianchuan Gao | Jialiang Hua | Qihang Wu | Paula Wu

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Background

- Breast cancer: most common invasive cancer in women around the world
- Early accurate diagnosis can greatly improve prognosis
- Logistic model and logistic-LASSO model
- Estimation
 - Newton-Raphson algorithm
 - Pathwise coordinate-wise optimization algorithm



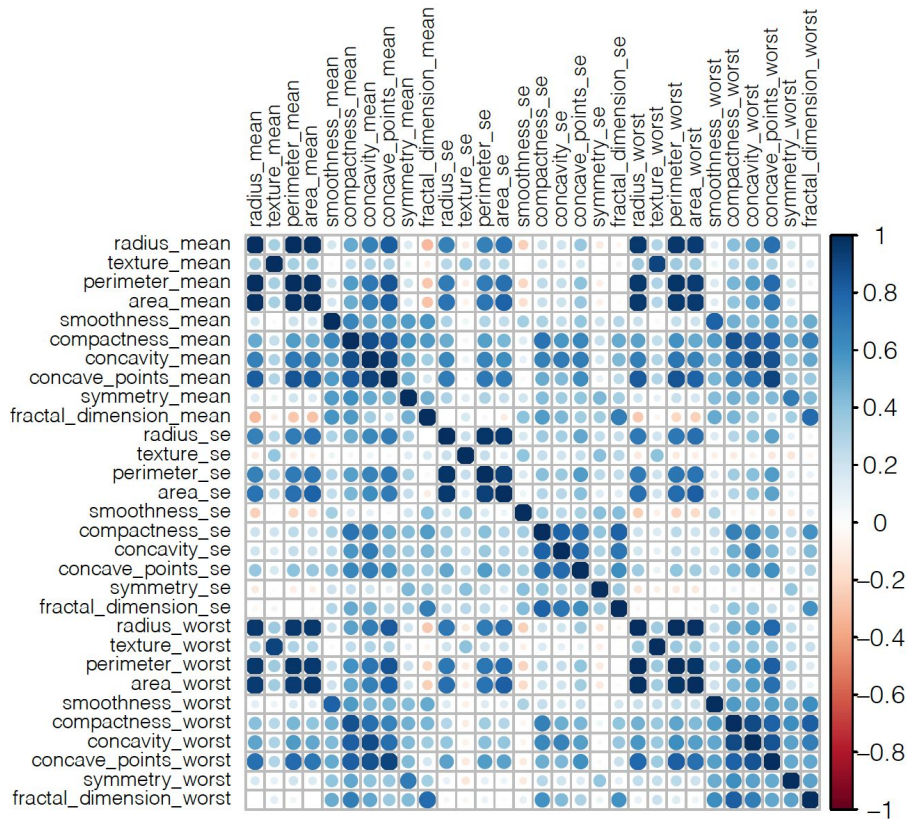
1.4M diagnosed
1.4 million women globally are diagnosed with breast cancer each year¹

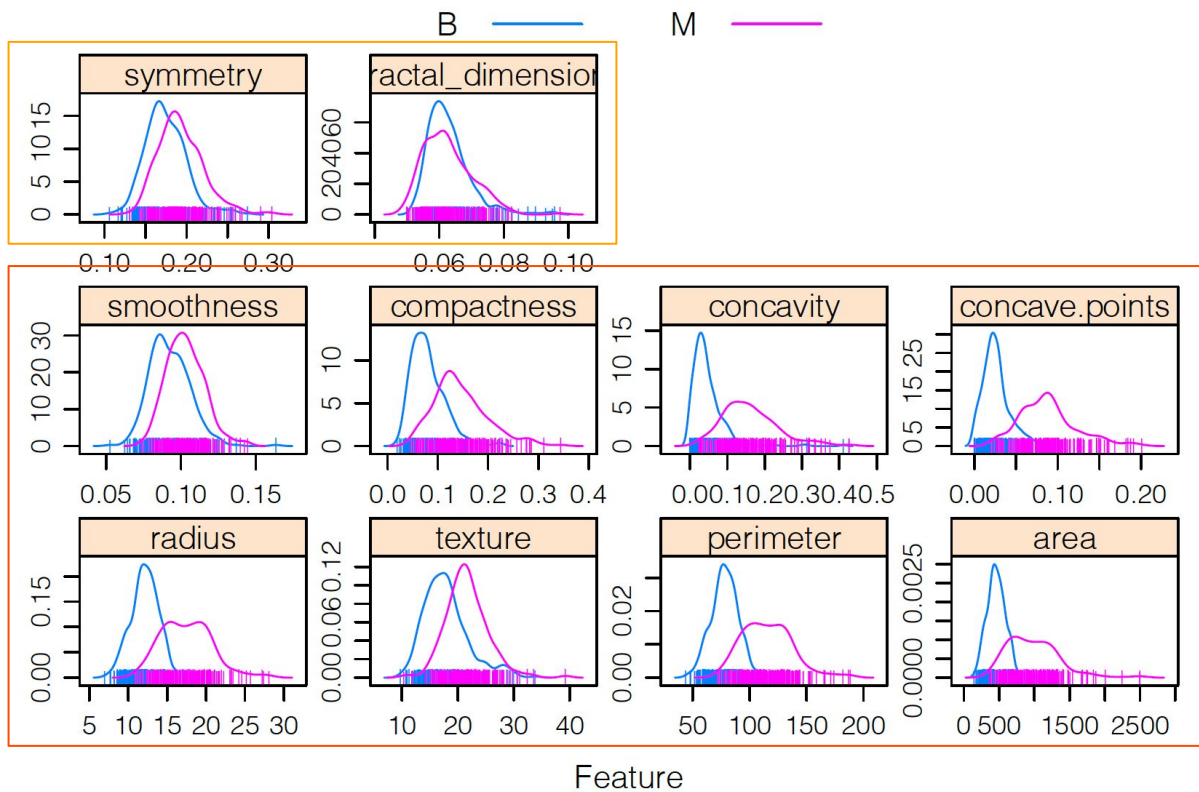
1.7M new cases
By 2020, there will be over 1.7 million new cases of breast cancer annually²

500,000 deaths
Globally, breast cancer causes more than 500,000 deaths each year³

10.5% of cancers
Breast cancer comprises 10.5% of all new cancers worldwide⁴

EDA





Newton-Raphson Algorithm

The logistic model can be defined as: $\log\left(\frac{\pi_i}{1 - \pi_i}\right) = \mathbf{X}\beta \longrightarrow \pi_i = \frac{e^{\mathbf{X}\beta}}{1 + e^{\mathbf{X}\beta}}$

The likelihood function : $L(\beta) = \prod_{i=0}^n \left(\frac{e^{\mathbf{X}\beta}}{1 + e^{\mathbf{X}\beta}}\right)^{y_i} \left(\frac{1}{1 + e^{\mathbf{X}\beta}}\right)^{1-y_i} \longrightarrow$ Log likelihood function: $l(\beta) = \sum_{i=0}^n (y_i * \mathbf{X}\beta - \log(1 + e^{\mathbf{X}\beta}))$

Gradient:
$$\nabla l(\beta) = \begin{pmatrix} \sum_{i=1}^n (y_i - \pi_i) \\ \sum_{i=1}^n x_{i1} \times (y_i - \pi_i) \\ \vdots \\ \sum_{i=1}^n x_{in} \times (y_i - \pi_i) \end{pmatrix}$$

Hessian Matrix:

$$\begin{aligned} \nabla^2 f(\beta) &= - \sum_{i=1}^n \begin{pmatrix} 1 \\ x_i \end{pmatrix} \begin{pmatrix} 1 & x_i \end{pmatrix} \pi_i (1 - \pi_i) \\ &= - \begin{pmatrix} \sum \pi_i (1 - \pi_i) & \sum x_i \pi_i (1 - \pi_i) \\ \sum x_i \pi_i (1 - \pi_i) & \sum x_i^2 \pi_i (1 - \pi_i) \end{pmatrix} \end{aligned}$$

With these parameters, we can apply the Newton-Raphson algorithm to calculate a set of beta using this equation:

$$\beta_{i+1} = \beta_i - [\nabla^2 l(\beta_i)]^{-1} \nabla l(\beta_i)$$

Step-halving and re-direction modification:

Ensure the likelihood is increasing and the ascent direction at β_i

Newton-Raphson Result

- Test for the first 10 features.
- Compare to glm results, outcomes are very close.
- Also test for all 30 features, result is not ideal due to computation burden when calculating the inverse of the Hessian matrix.

	Coefficients
Intercept	0.487
Radius Mean	-7.221
Texture Mean	1.654
Perimeter Mean	-1.737
Area Mean	14.005
Smoothness Mean	1.075
Compactness Mean	-0.077
Concavity Mean	0.675
Concave Point Mean	2.593
Symmetry Mean	0.446
Fractal Dimension Mean	-0.482

(Intercept)	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
0.48701675	-7.22185053	1.65475615	-1.73763027	14.00484560	1.07495329
compactness_mean	concavity_mean	concave_points_mean	symmetry_mean	fractal_dimension_mean	
-0.07723455	0.67512313	2.59287426	0.44625631	-0.48248420	

Coordinatewise descent (CD) Lasso

- High-dimensional covariates; Standardize
- Soft threshold function: $S(\hat{\beta}, \gamma) = \text{sign}(\hat{\beta}) (|\hat{\beta}| - \gamma)_+$
- CD algorithm: update β_j repeatedly for $j = 1, \dots, p, 1, \dots, p$
- For different weights w_i : $\tilde{\beta}_j(\gamma) = \frac{S(\sum_i^n w_i x_{i,j} (Z_i - \tilde{Z}_i^{(-j)}), \gamma)}{\sum_i^n w_i x_{i,j}^2}$
- Working weights $w_i > 0$: $\tilde{\pi}_i(1 - \tilde{\pi}_i)$
- Working response Z_i : $X_i \tilde{\beta} + \frac{y_i - \tilde{\pi}_i}{\pi_i(1 - \pi_i)}$

Taylor expansion around current estimates:

$$l(\beta) = -\frac{1}{2n} \sum_{i=1}^n w_i (Z_i - X_i \beta)^2$$

- Object Function: $\min_{(\beta)} L(\beta, \lambda) = \left\{ -l(\beta) + \lambda \sum_{j=0}^p |\beta_j| \right\}$

```
# Soft Threshold function
sf <- function(beta, lambda) {
  beta <- ifelse(lambda < abs(beta),
    ifelse(beta > 0, beta - lambda, beta + lambda), 0)
  return(beta)
}

# Coordinate-wise LASSO with fixed lambda
cd_lasso <- function(dat, y, betavec, lambda, maxier = 2000, tol = 1e-10) {
  x <- dat # n * (p + 1) matrix, standardized
  i <- 0
  objfun <- 0
  prev_objfun <- -Inf # ensure iterations
  res <- c(0, objfun, betavec)

  while (i < maxier && abs(objfun - prev_objfun) > tol) {
    i <- i + 1
    prev_objfun <- objfun

    for (j in 1:length(betavec)) {
      u <- x %*% betavec
      pi <- exp(u) / (1 + exp(u))
      # working weights
      w <- pi * (1 - pi)
      w <- ifelse(w < 1e-5, 1e-5, w)
      # working response
      z <- x %*% betavec + (y - pi) / w
      z_dej <- x[, -j] %*% betavec[-j]
      betavec[j] <-
        sf(sum(w * x[, j] * (z - z_dej)), lambda) / (sum(w * x[, j]^2))
    }
    objfun <-
      sum(w * (z - x %*% betavec)^2) / (2 * dim(x)[1]) + lambda * sum(abs(betavec))
    if (is.na(objfun)) {break}

    res <- rbind(res, c(i, objfun, betavec))
  }

  return(res)
}
```

LASSO - Pathwise Coordinate-wise optimization

1. Select a λ_{\max} for all the estimate $\beta = 0$
2. Compute the solution with a sequence of descending λ from maximum
3. Initialize coordinate descent algorithms by the calculated estimate β from previous λ
4. Find the optimal solution by comparing the objective function:

$$\min_{(\beta)} L(\beta, \lambda) = \left\{ -l(\beta) + \lambda \sum_{j=0}^p |\beta_j| \right\}$$

```
> max(t(bc_scale2_x) %*% bc_scale2_y)
[1] 218.1238
```

```
pathwise_cd_lasso <- function(dat, y, betavec, lambda) {
  sort(lambda, decreasing = TRUE)
  pathwise_res <- NA

  for (j in 1:length(lambda)) {
    cd_results <- cd_lasso(dat, y, betavec, lambda[j])

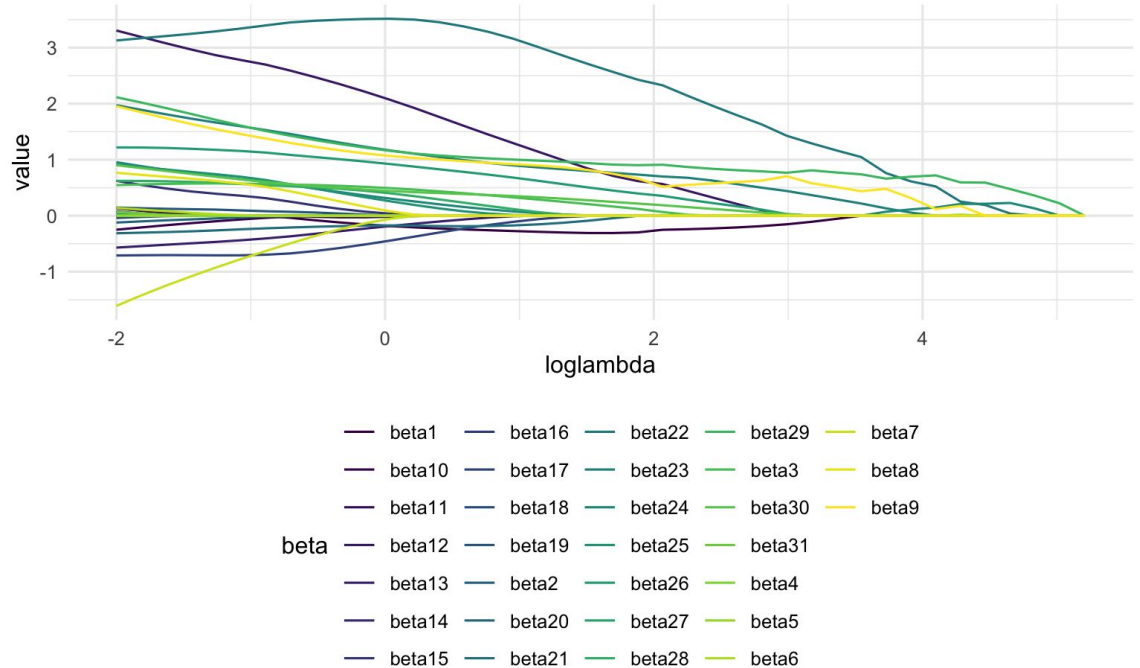
    # warm start
    min_objfun_ind <- which.min(cd_results[-1, 2]) + 1
    betavec <- cd_results[min_objfun_ind, -c(1, 2)]
    objfun <- cd_results[min_objfun_ind, 2]

    pathwise_res <- rbind(pathwise_res,
                          c(j, lambda = lambda[j], obj = objfun,
                            beta = betavec))
  }

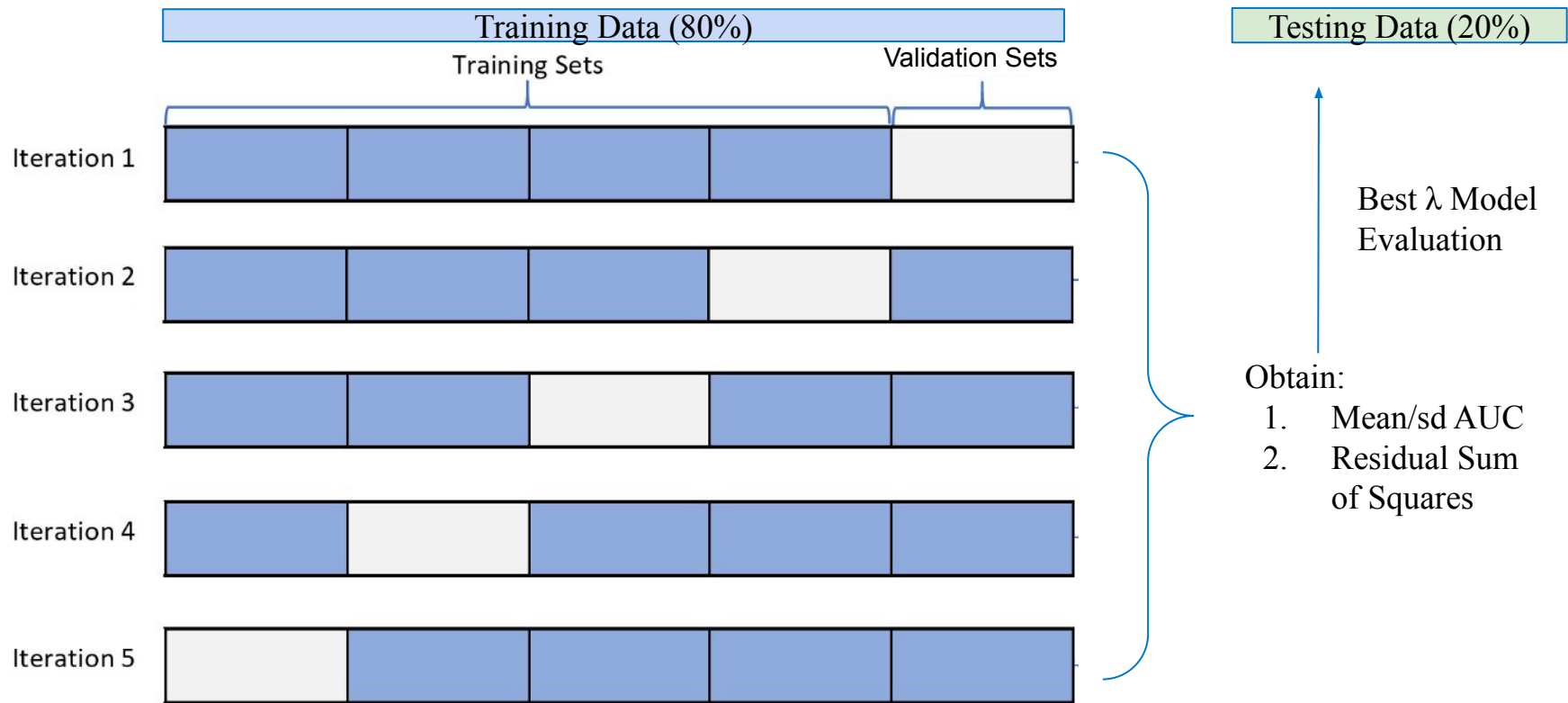
  return(pathwise_res[-1, ])
}
```


LASSO - Pathwise Coordinate-wise optimization

- Solution for each coefficients β under different descending λ
- Roughly, λ we select is 0.135 but need further cross-validation



Cross Validation - Overview

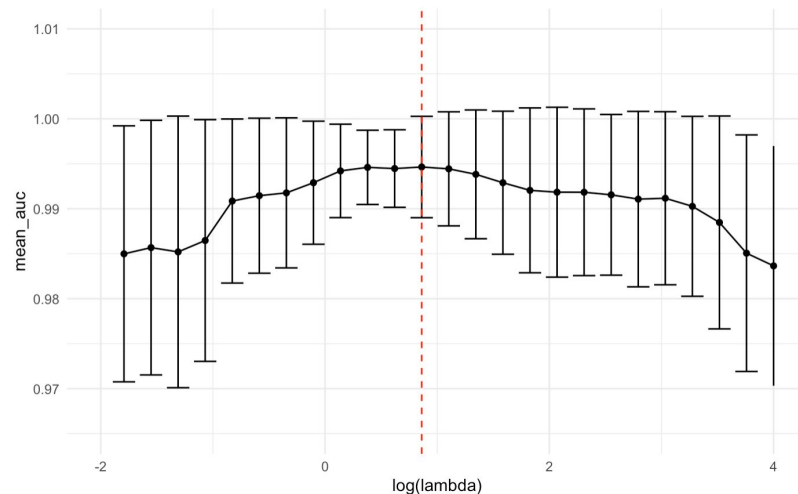


Cross Validation - Steps

1. Select 30 equally spaced λ from range $e^{(4, -3)}$
 - a. Upper bound: arbitrary, a λ value that is large but not large enough to force all β 's become 0.
2. For each λ , run the 5-fold CV. For each fold:
 - a. Run Coordinate-wise Lasso on training sets
 - b. Extract current “best” beta (i.e. the last row) from the results
 - c. Make prediction and calculate AUC, RSS against validation sets
3. Calculate mean and std-dev of AUC and mean RSS for each λ

Results & Discussion - Optimal vs. Full Models

- Optimal λ : the λ that maximize the mean AUC
 - ~ 2.3681
- Test against testing data:
 - Optimal Model: $\lambda_{\text{optimal}} = 2.3681$
 - Full Model: $\lambda = 0$
- Compare the predicted outcome vs. actual outcome \rightarrow calculate AUC
- Full model: AUC = 1
- Optimal model: AUC = 0.9989



Limitations

- Our Newton-Raphson method still use the inverse of Hessian matrix, which is not accurate when p is large
 - Try alternatives that replace Hessian matrix
- During the cross-validation process, we select a wide range of λ with only sparse data points.
 - Try a denser model with narrower range for more precise predict of λ

Questions?

Reference

[1] Data: breast_cancer.csv

[2] CV illustration:

<https://towardsdatascience.com/cross-validation-k-fold-vs-monte-carlo-e54df2fc179b>

Thank you!