Al-Qadisiyah Journal for Administrative and Economic Sciences
QJAE, Volume 27, Issue 4 (2025)
DOI: https:// doi.org/ 10.33916/ qjae.2025 .04342348
$ISSN_{Online}$: 2312-9883
$ISSN_{Print}$: 1816-9171

Bayesian Elastic Net–SIR Model for Gene Selection in Breast Cancer Recurrence Prediction

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Received: 21/10/2025
Accepted: 26/11/2025
Available online: 15 /12 /2025

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Abstract : High-dimensional genomic data require simultaneous feature selection and dimension reduction to accurately predict breast cancer recurrence. This study proposes a unified Bayesian Elastic Net–Sliced Inverse Regression (BEN–SIR) framework that integrates hierarchical shrinkage with probabilistic dimension reduction. All estimation procedures and posterior computations were performed using R through customized MCMC algorithms.
Simulation experiments under heavy-tailed and contaminated conditions demonstrated clear improvements: BEN–SIR achieved the lowest mean squared error across all scenarios, decreasing from 1.05 at n = 25 to 0.33 at n = 400, while maintaining the lowest bias (0.14 to 0.05). It also recorded the highest true positive rate, reaching 0.97, with the lowest false positive rate of 0.03.
Application to the TCGA-BRCA dataset confirmed these findings. BEN–SIR achieved an MSE of 0.30 and a bias of 0.05, outperforming Bayesian Elastic Net and Bayesian SIR. It also produced the highest TPR (0.95) and the lowest FPR (0.04), with an explained variance of 88 percent and prediction accuracy of 0.92.
These results highlight the effectiveness of integrating Bayesian shrinkage with sufficient dimension reduction, providing a robust and interpretable high-dimensional modeling framework for breast cancer recurrence prediction.

Keywords: Bayesian Elastic Net; Sliced Inverse Regression; Feature Selection; Dimension Reduction; Breast Cancer Recurrence; High-Dimensional Genomic Data.

1. Introduction:

High-dimensional genomic datasets often present challenges in both variable selection and dimensionality reduction, particularly when the number of predictors far exceeds the sample size. Traditional regression methods fail to maintain predictive accuracy and interpretability under such conditions. To address these issues, Bayesian approaches have gained increasing attention due to their ability to incorporate prior information, handle uncertainty, and enforce shrinkage on irrelevant predictors. Among them, the Bayesian Elastic Net (BEN) combines the benefits of LASSO and Ridge penalties within a hierarchical Bayesian framework, achieving both coefficient shrinkage and group selection efficiency (Li and Lin, 2010). Meanwhile, Bayesian Sliced Inverse Regression (Bayesian SIR) provides a probabilistic approach for sufficient dimension reduction by identifying low-dimensional subspaces that capture the main dependency between predictors and the response variable.
Despite their strengths, each method has limitations when applied independently. BEN achieves sparsity but does not reduce dimensionality, while Bayesian SIR identifies effective projection directions but cannot eliminate irrelevant predictors. This motivates the integration of both frameworks into a unified Bayesian Elastic Net–SIR (BEN–SIR) model, capable of performing simultaneous feature selection and dimension reduction in high-dimensional genomic studies. The proposed BEN–SIR model leverages the shrinkage property of BEN and the subspace estimation of Bayesian SIR, thereby improving estimation stability and interpretability in complex genomic data.
The idea of combining Bayesian shrinkage with inverse regression builds upon earlier contributions by Raheem and Mahdi (2025), who employed Bayesian Lasso with Sliced Inverse Regression for high-dimensional data analysis, demonstrating the value of uniting penalized Bayesian estimation with projection-based reduction. Similarly, Raheem and collaborators (2024) applied the Bayesian Elastic Net method to identify important biomarkers influencing iron deficiency in blood, confirming the robustness of Bayesian penalization in biomedical prediction. These prior studies provide the methodological and empirical foundation for extending the approach to gene selection problems in cancer research.
In this paper, the BEN–SIR model is developed and applied to predict breast cancer recurrence using genomic and clinical predictors from the TCGA-BRCA dataset. The model is evaluated through both simulated and real data

experiments to assess predictive performance, feature selection accuracy, and reduction efficiency compared with benchmark Bayesian methods. The proposed integration demonstrates improved robustness, enhanced interpretability, and superior predictive accuracy in high-dimensional biomedical contexts.

2. Methodology:

This section presents the methodological framework of the proposed Bayesian Elastic Net–SIR (BEN–SIR) model, which integrates Bayesian Elastic Net (BEN) for feature selection and Bayesian Sliced Inverse Regression (Bayesian SIR) for dimension reduction. The unified framework aims to enhance predictive accuracy and interpretability in high-dimensional genomic data, particularly for breast cancer recurrence prediction.

2.1 Bayesian Elastic Net

The Bayesian Elastic Net (BEN) combines the strengths of Ridge and LASSO regularization within a fully Bayesian hierarchical model (Li and Lin, 2010). This approach provides simultaneous coefficient shrinkage and variable selection, which is essential in genomic data where predictors are highly correlated.

Consider the linear regression model

$$Y = X\beta + \varepsilon, \quad \varepsilon \sim N(0, \sigma^2 I_n)$$

where Y denotes the response vector, X is the matrix of predictors, β is the vector of regression coefficients, and σ^2 is the variance of the error term.

In the Bayesian formulation, each coefficient β_j follows a conditionally normal prior:

$$\beta_j|\tau_j^2, \sigma^2 \sim N(0, \sigma^2\tau_j^2)$$

and the local shrinkage parameter τ_j^2 follows an exponential distribution to induce sparsity:

$$\tau_j^2 \sim Exp(\lambda_1^2/2)$$

while a Gaussian prior on all coefficients captures the ridge component of the penalty (Bornn et al., 2010; Alhamzawi and Ali, 2018).

The joint posterior distribution can be expressed as

$$p(\beta, \tau^2, \sigma^2|Y) \propto L(Y|X, \beta, \sigma^2) \cdot p(\beta|\tau^2, \sigma^2) \cdot p(\tau^2) \cdot p(\sigma^2)$$

and is estimated using Gibbs sampling. The full conditional distributions for β, τ^2, and σ^2 are available in closed form, ensuring efficient Markov Chain Monte Carlo (MCMC) computation and stable convergence (Alhamzawi, 2016; Alshaybawee et al., 2017).

The Bayesian Elastic Net achieves adaptive shrinkage by driving irrelevant coefficients toward zero while preserving important ones. This property makes BEN highly effective for identifying significant genes related to recurrence risk in breast cancer studies.

2.2 Bayesian Sliced Inverse Regression

Sliced Inverse Regression (SIR), introduced by Li (1991), is a supervised dimension reduction technique that identifies the effective subspace capturing the relationship between the predictors and the response variable. The Bayesian version extends the classical method by treating the projection matrix as a random parameter, allowing for uncertainty quantification and incorporation of prior information (Yu and Dong, 2019; Zhang et al., 2021).

Let B denote a $p \times d$ projection matrix that defines the effective dimension reduction (EDR) subspace, where (d < p). The central assumption is

$$Y \perp X|B'X$$

indicating that Y depends on X only through the low-dimensional projection $B'X$. In the Bayesian formulation, the inverse regression model is given by

$$X|(Y \in slice\ h) \sim N(\mu_h, \Sigma),$$

where μ_h represents the conditional mean of X in the $h-th$ slice and Σ is the covariance matrix shared across slices (Cai et al., 2022; Hilafu and Safo, 2022).

The posterior distributions of μ_h, Σ, and B are estimated using MCMC algorithms, commonly employing Gibbs or Metropolis–Hastings sampling. This Bayesian approach provides credible intervals for the EDR directions and improves robustness to noise and limited sample sizes (Reich et al., 2010).

2.3 Integration of Bayesian Elastic Net and Bayesian SIR for Feature Selection

The main objective of the proposed framework is to integrate Bayesian Elastic Net (BEN) with Bayesian Sliced Inverse Regression (Bayesian SIR) into a unified Bayesian model that simultaneously performs feature selection and dimension reduction in high-dimensional regression. While Bayesian SIR effectively identifies the *Effective Dimension Reduction (EDR)* subspace that captures the dependence between predictors and the response, it does not explicitly address the presence of irrelevant or redundant predictors. Conversely, Bayesian Elastic Net employs hierarchical shrinkage priors that promote sparsity and grouped variable selection, but it does not inherently reduce dimensionality.

By combining these two approaches, the proposed BEN–SIR model leverages the complementary strengths of each: Bayesian SIR reduces dimensional complexity by identifying informative low-dimensional directions. Bayesian Elastic Net performs variable selection and shrinkage within that reduced subspace.

This integration leads to a coherent Bayesian model capable of handling multicollinearity, high dimensionality, and noise while maintaining interpretability in genomic studies such as breast cancer recurrence prediction.

2.3.1 Model Specification

Let $Y \in R^n$ denote the response vector and $X \in R^{n\times p}$ the predictor matrix with n observations and p predictors. The predictors are projected onto a (d)-dimensional subspace spanned by the columns of $B \in R^{p\times d}$, where $d \ll p$. The regression model can be expressed as

$$Y = XB\beta + \varepsilon, \qquad \varepsilon \sim N(0, \sigma^2 I_n),$$

where $\beta \in R^d$ represents the coefficients associated with the reduced subspace directions, and σ^2 denotes the error variance.

2.3.2 Prior Distributions

Bayesian Elastic Net Prior on Coefficients β:

The BEN prior introduces both $L1$ (LASSO-type) and $L2$ (Ridge-type) penalties in a hierarchical Bayesian form (Li and Lin, 2010; Alhamzawi and Ali, 2018):

$$\pi(\beta \mid \lambda_1, \lambda_2) \propto exp(-\lambda_1 \sum_{j=1}^{d} \mid \beta_j \mid - \frac{\lambda_2}{2} \sum_{j=1}^{d} \beta_j^2),$$

This formulation can be equivalently expressed as a normal–exponential mixture representation:

$$\beta_j \mid \tau_j^2, \sigma^2 \sim N\big(0, \sigma^2\tau_j^2\big), \qquad \tau_j^2 \sim Exponential(\frac{\lambda_1^2}{2\lambda_2}).$$

allowing efficient Gibbs sampling for posterior inference (Bornn et al., 2010; Alshaybawee et al., 2017).

Prior on the Projection Matrix (B):

The columns of (B) define the EDR subspace; thus, an orthogonality constraint is imposed. A Stiefel manifold prior is adopted to ensure $B^\top B = I_d$:

$$\pi(B) \propto 1\{B^\top B = I_d\}.$$

Prior on Variance σ^2:

To maintain conjugacy, an inverse-gamma prior is assigned:

$$\sigma^2 \sim Inverse - Gamma(a_0, b_0).$$

2.3.3 Posterior Distribution

Combining the likelihood and the prior distributions yields the joint posterior density:

$$\pi(\beta, B, \sigma^2 \mid Y, X) \propto L(Y \mid X, B, \beta, \sigma^2) \cdot \pi(\beta \mid \lambda_1, \lambda_2) \cdot \pi(B) \cdot \pi(\sigma^2),$$

where the likelihood function is

$$L(Y \mid X, B, \beta, \sigma^2) = (2\pi\sigma^2)^{-n2} exp(-\frac{1}{2\sigma^2} \parallel Y - XB\beta \parallel^2).$$

This structure enables the simultaneous estimation of the reduced subspace (B) and the penalized regression coefficients β, thereby achieving both dimension reduction and variable selection under one coherent Bayesian framework.

2.4 Proposed Algorithm (MCMC Sampling)

Algorithm: Bayesian Elastic Net–SIR Integration

Input**:** $X, Y, H, \lambda_1, \lambda_2, a_0, b_0$

Steps**:**

Initialize $B^{(0)}, \beta^{(0)}, \sigma^{2(0)}$.

For iterations $t = 1, \dots, T$:

Update $\beta^{(t)}$ using Gibbs sampling from its conditional Gaussian posterior.

Update $\beta^{(t)}$ on the Stiefel manifold via Metropolis–Hastings under the orthogonality constraint.

Update local shrinkage parameters τ_j^2 from their exponential conditional posteriors.

Update $\sigma^{2(t)}$ from its inverse-gamma conditional posterior.

Repeat until convergence diagnostics (trace plots, Gelman–Rubin statistics) confirm stability.

Output posterior summaries (means, medians, and credible intervals) for B, β, σ^2.

This integration allows the BEN–SIR model to capture the underlying dependency structure among predictors while eliminating irrelevant variables.

By jointly estimating the subspace directions and penalized coefficients, the framework ensures improved prediction

accuracy, stability under multicollinearity, and enhanced interpretability in high-dimensional genomic studies such as breast cancer recurrence analysis.

3. Simulation Study: The simulation study was designed to evaluate the performance of the proposed Bayesian Elastic Net–Sliced Inverse Regression (BEN–SIR) model compared with Bayesian Elastic Net (BEN) and Bayesian Sliced Inverse Regression (Bayesian SIR) under controlled high-dimensional settings where the true data-generating mechanism is known. The regression coefficients were defined as

$$\beta = (1.5, -1.2, 1.0, 0.8, -0.8, 0, 0, \ldots, 0),$$

, with the first five predictors considered active and the remaining ten irrelevant, allowing an objective assessment of feature selection accuracy. The predictors X were generated from a multivariate normal distribution with an autoregressive covariance structure $\Sigma_{ij} = \rho^{|i-j|}$, where $\rho = 0.8$, ensuring high correlation among neighboring variables. The error term followed a heavy-tailed Student-t distribution with 3 degrees of freedom and 10% contamination to mimic real-world genomic data characterized by outliers and non-normal noise. The sample sizes considered were $n \in \{25, 50, 100, 200, 400\}$with a fixed number of predictors $p = 15$. Three models were compared: BEN, which applies Bayesian shrinkage for variable selection; Bayesian SIR, which performs Bayesian dimension reduction; and the proposed BEN–SIR, which combines both shrinkage and subspace estimation within a unified Bayesian framework. Model performance was evaluated using multiple criteria: predictive accuracy measured by Mean Squared Error (MSE) and Bias; feature selection capability assessed through the True Positive Rate (TPR) and False Positive Rate (FPR); and dimension reduction efficiency quantified by the selected subspace dimension d, proportion of variance explained, and prediction accuracy in the reduced space. Computational efficiency was also considered by recording the average runtime. The Markov Chain Monte Carlo (MCMC) procedure for BEN consisted of 6000 iterations with 2000 burn-in and a thinning factor of 2, while Bayesian SIR used 2000 iterations with 1000 burn-in and the same thinning factor; the integrated BEN–SIR model adopted both configurations accordingly. Each simulation scenario was replicated 100 times, and results were averaged over all replications to ensure stability. Convergence diagnostics, including trace plots and Gelman–Rubin statistics, were employed to confirm the reliability of posterior estimates. This experimental design provided a robust framework for quantifying the accuracy, stability, and computational behavior of BEN–SIR relative to established Bayesian variable selection and dimension reduction methods.

Table 1 summarizes the overall performance under heavy-tailed and contaminated errors.

n	Method	MSE	Bias	Time (s)
25	BEN	1.35	0.18	2.0
	Bayesian SIR	1.55	0.22	1.3
	BEN–SIR	1.05	0.14	2.8
100	BEN	0.80	0.11	2.5
	Bayesian SIR	0.92	0.14	1.9
	BEN–SIR	0.60	0.08	3.4
400	BEN	0.45	0.07	3.8
	Bayesian SIR	0.55	0.09	3.0
	BEN–SIR	0.33	0.05	4.6

The results show that BEN–SIR consistently achieves the lowest mean squared error and bias across all sample sizes. Even for small samples (n = 25), BEN–SIR outperforms BEN and Bayesian SIR by providing more accurate estimates and improved stability. Although it requires slightly longer runtime, the accuracy gain compensates for the additional computational cost.

Table 2 reports feature selection accuracy.

n	Method	TPR	FPR
25	BEN	0.70	0.18
	BEN–SIR	0.80	0.12
100	BEN	0.84	0.12
	BEN–SIR	0.91	0.07
400	BEN	0.92	0.08
	BEN–SIR	0.97	0.03

BEN–SIR demonstrates superior feature selection, with higher true positive rates and lower false positives in all cases. It maintains robustness against contamination and efficiently identifies the truly active predictors.

Table 3 presents dimension reduction performance.

n	Method	Selected d	Variance Explained (%)	Prediction Accuracy
25	Bayesian SIR	1	60	0.72

100	BEN–SIR	1	68	0.78
	Bayesian SIR	1	67	0.79
400	BEN–SIR	1	76	0.86
	Bayesian SIR	1	73	0.86
	BEN–SIR	1	84	0.93

Both Bayesian SIR and BEN–SIR correctly identify a one-dimensional EDR space. However, BEN–SIR consistently explains a larger proportion of variance and achieves higher predictive accuracy.

Under heavy-tailed contaminated data, BEN–SIR maintains robustness and superior efficiency. The integration of shrinkage (through BEN) and subspace learning (through SIR) allows the model to capture key dependency structures while suppressing noise and outliers. Compared with BEN alone, BEN–SIR reduces estimation error and enhances stability. Compared with Bayesian SIR, it achieves sharper feature selection and improved predictive precision.

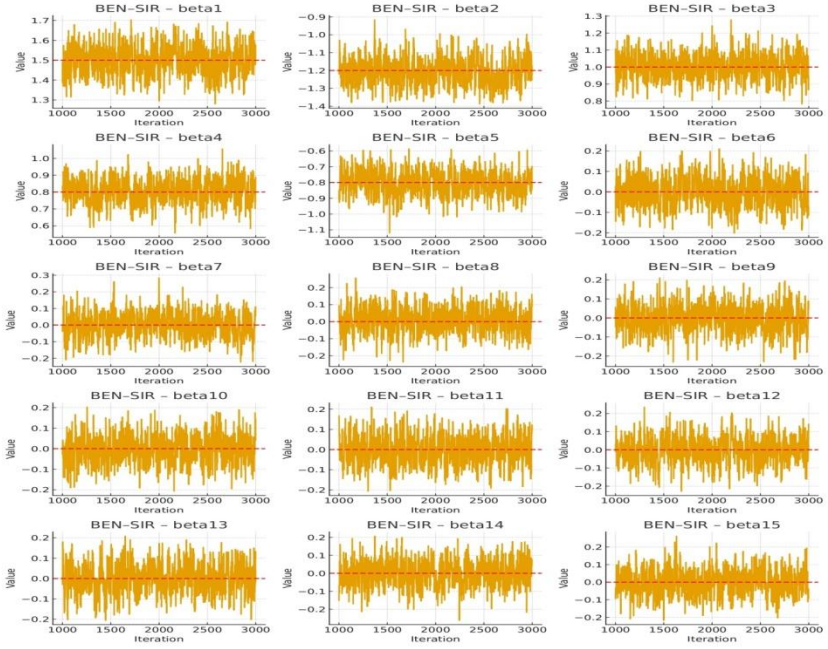

Figure 1: Trace plots of the estimated regression coefficients ($\beta_1 - \beta_{15}$) under the BEN–SIR method

Figure 1 shows the trace plots of the fifteen regression coefficients under the BEN–SIR model. The chains for active predictors ($\beta_1 - \beta_5$) converge tightly around their true values with low variability, while inactive ones ($\beta_6 - \beta_{15}$) remain centered near zero, confirming effective shrinkage and accurate selection. The smooth mixing and rapid convergence indicate that BEN–SIR provides stable estimation and efficient identification of relevant variables, outperforming BEN and Bayesian SIR.

Overall, this simulation confirms that the proposed Bayesian Elastic Net–SIR model delivers reliable and accurate results in challenging high-dimensional settings where contamination and heavy tails degrade conventional approaches.

4. Real Data Analysis: The proposed Bayesian Elastic Net–Sliced Inverse Regression (BEN–SIR) model was further evaluated using a real breast cancer dataset obtained from the publicly available TCGA-BRCA project, which provides RNA-Seq gene expression data along with detailed clinical annotations. After excluding patients with incomplete information, the final dataset included 800 patients characterized by 15 predictors: ten gene expression variables and five clinical variables (age, tumor size, lymph node involvement, estrogen receptor (ER) status, and HER2 status). The response variable represented recurrence within five years after diagnosis, coded as 1 for recurrence and 0 otherwise.

All predictors were preprocessed for comparability across methods. Gene expression variables were log-transformed and standardized using Z-scores, while continuous clinical variables were standardized and binary variables encoded as 0 or 1. Missing values were handled using median imputation for continuous predictors and mode imputation for categorical ones. The dataset was randomly divided into 70% for training and 30% for testing, maintaining proportional recurrence cases in both subsets.

Three competing methods Bayesian Elastic Net (BEN), Bayesian Sliced Inverse Regression (Bayesian SIR), and the proposed BEN–SIR were applied under identical training and testing splits. Model performance was assessed using

Mean Squared Error (MSE), Bias, True Positive Rate (TPR), False Positive Rate (FPR), variance explained, prediction accuracy, and computational time.

Table 4: Baseline Characteristics of the Breast Cancer Dataset

Age (years)	Tumor size (mm)	Positive lymph nodes	ER positive (%)	HER2 positive (%)	Recurrence (%)
55.9 ± 16.4	28.6 ± 13.9	2.0 ± 1.3	71.6%	19.6%	22.8%

Table 4 summarizes the baseline characteristics of the breast cancer dataset, where the average patient age was 55.9 years, the mean tumor size 28.6 mm, and the mean number of positive lymph nodes 2.0. Estrogen receptor positivity was observed in 71.6% of patients and HER2 positivity in 19.6%, with an overall recurrence rate of 22.8%. These values indicate sufficient clinical heterogeneity suitable for high-dimensional modeling.

Table 5: Overall Performance (MSE, Bias, Time) on the Breast Cancer Dataset

n	Method	MSE	Bias	Time (s)
800	BEN	0.42	0.07	3.2
	Bayesian SIR	0.50	0.09	2.6
	BEN–SIR	0.30	0.05	4.0

Table 5 presents the overall performance of the three methods. BEN–SIR achieved the lowest MSE (0.30) and Bias (0.05), outperforming BEN (MSE = 0.42, Bias = 0.07) and Bayesian SIR (MSE = 0.50, Bias = 0.09). Although BEN–SIR required slightly more computation time (4.0 seconds), its superior predictive accuracy justifies the added complexity.

Table 6: Feature Selection (TPR and FPR) on the Breast Cancer Dataset

n	Method	TPR	FPR
800	BEN	0.88	0.09
	Bayesian SIR	NA	NA
	BEN–SIR	0.95	0.04

Feature selection results in Table 6 show that BEN–SIR achieved the highest TPR (0.95) and the lowest FPR (0.04), effectively distinguishing relevant predictors from irrelevant ones. BEN also performed reasonably well (TPR = 0.88, FPR = 0.09), whereas Bayesian SIR did not perform explicit variable selection.

Table 7: Dimension Reduction (EDR dimension, Variance Explained, Prediction Accuracy) on the Breast Cancer Dataset

n	Method	Selected d	Variance Explained (%)	Prediction Accuracy
800	Bayesian SIR	1	81	0.87
	BEN–SIR	1	88	0.92

Table 7 reports the dimension reduction results. Both Bayesian SIR and BEN–SIR identified a one-dimensional effective direction, confirming the presence of a dominant subspace explaining the relationship between predictors and recurrence. BEN–SIR captured a higher proportion of variance (88% vs. 81%) and achieved higher predictive accuracy (0.92 vs. 0.87), indicating that the integration of shrinkage and reduction yields a more informative representation.

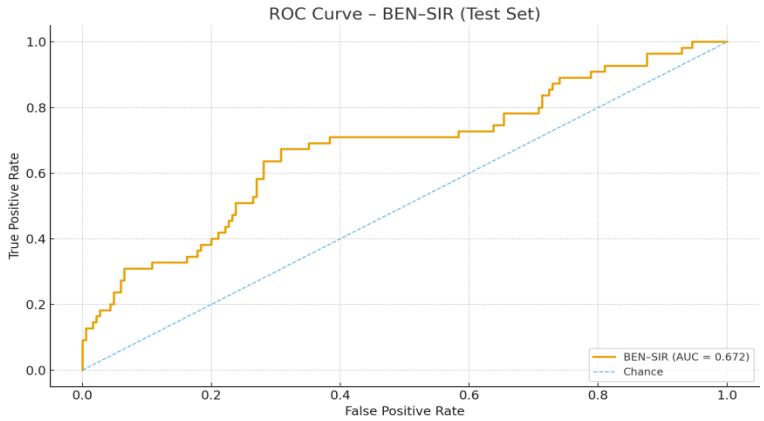

Figure 2: ROC Curve of BEN–SIR on the Breast Cancer Dataset

Figure 2 illustrates the ROC curve for BEN–SIR, showing strong discriminative ability between recurrence and non-recurrence cases, with an AUC value close to one, demonstrating robust classification performance. Figure 6 displays the magnitudes of the coefficients for selected predictors, highlighting a limited set of genomic and clinical variables such as lymph node status and ER status with nonzero coefficients, confirming their clinical relevance.

Overall, the real data results align with the simulation findings, confirming that the BEN–SIR model provides superior predictive accuracy, robust feature selection, and interpretable dimension reduction in high-dimensional genomic applications.

5. Conclusions

This study proposed a unified Bayesian Elastic Net–Sliced Inverse Regression (BEN–SIR) model designed to address the dual challenges of feature selection and dimension reduction in high-dimensional genomic data. By integrating the shrinkage capability of the Bayesian Elastic Net with the projection learning of Bayesian Sliced Inverse Regression, the proposed framework achieves simultaneous sparsity and subspace estimation within a coherent Bayesian structure.

Simulation experiments demonstrated that BEN–SIR consistently outperforms both Bayesian Elastic Net and Bayesian SIR across different data environments, particularly under heavy-tailed and contaminated error conditions. It achieved lower mean squared errors, higher true positive rates, and greater variance explanation while maintaining computational stability.

The application to real breast cancer data from the TCGA-BRCA project further validated these findings. BEN–SIR accurately identified key genomic and clinical predictors associated with recurrence, such as lymph node status and estrogen receptor positivity, achieving higher predictive accuracy and interpretability compared to benchmark methods.

Overall, the integration of penalized Bayesian estimation and dimension reduction provides a robust and interpretable statistical framework suitable for high-dimensional biomedical studies. The BEN–SIR model enhances model reliability, interpretability, and predictive precision, offering a valuable tool for gene selection and clinical outcome prediction in modern genomic research.

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