# Sparse Bayesian Predictive Modelling of Tumor Response from Radiomic Data

Shirin Golchi

McGill University, Montréal, QC.

Collaborators: Sahir Bhatnagar, Janet Fu, Reza Forghani

#### Context and objectives

- Context: radiomic data for characterization of head and neck squamous cell carcinoma (HNSCC)
- A main objective in oncology: creation of a standardized set of criteria to predict tumor response to treatment;
- Radiomic features for characterization of HNSCC in addition to the traditional use of imaging;
- Image analysis algorithms extract mathematically defined features of the tumor's appearance giving rise to high-dimensional matrix covariates

#### **Radiomic features**

"Radiomics: Images Are More than Pictures, They Are Data" [Gillies et al., 2015]



#### Data

- Retrospective study of 605 patients diagnosed with primary pathology proven HNSCC with
- Tumor sites: 164 arising from oral cavity (OC), 200 oropharynx (OP), and 241 from larynx or hypopharynx (LHP)
- Outcome: lymph node metastasis (LN) (+/-)
- An important risk factor: Human Papilloma Virus (HPV) status (+/-)
- Covariates: smoking, drinking, T stage
- Radiomic features: 36

#### Data structure and challenges

- Dimensionality of the features matrix; only a few may be useful predictors – need efficient variable selection techniques
- Heterogeneity among tumor sites site-stratified variable selection and inference
- Disproportionately large volume of missing data variable selection and inference while dealing with missing data

#### What's currently done

- Random Forest classifiers/Lasso: no uncertainty estimates
- Decision of which features are the "most" important requires an arbitrary threshold
- Site-stratified analyses: not capable of borrowing information
- Imputation of missing values in a pre-processing step: under-representation of uncertainty

#### The model

- Bayesian hierarchical model for n = 1, ..., N patient data,

$$\begin{split} \widehat{\mathbf{y}_{1n}} &\sim \mathsf{Bernoulli}(\pi_{1n}), \quad \overbrace{\mathbf{y}_{2n}}^{\mathsf{HPV}} \sim \mathsf{Bernoulli}(\pi_{2n}) \\ \mathsf{logit}(\pi_{1n}) &= \phi \pi_{2n} + \mathbf{z}_n \boldsymbol{\eta}_1 + \mathbf{x}_n \boldsymbol{\beta}_{1s_n}, \\ \mathsf{logit}(\pi_{2n}) &= \mathbf{z}_n \boldsymbol{\eta}_2 + \mathbf{x}_n \boldsymbol{\beta}_{2s_n}, \end{split}$$

$$- s_n = 1, \ldots, S$$
 are the tumor sites,

- z<sub>n</sub> are a set of covariates (drinking, smoking and T-stage group)
- $-\mathbf{x}_n$  is the  $F \times 1$  vector of radiomic features

#### A word on sparse Bayesian regression

- A useful case study by Michael Betancourt [Betancourt, 2018]
- The direct translation of Lasso penalty to a prior (Laplace) doesn't quite equivalent;
- The Horseshoe prior [Carvalho et al., 2009] solves this by introducing global and a local scale parameters,

$$\beta_j \sim \mathcal{N}(\mathbf{0}, \tau^2 \lambda_j^2),$$
$$\underbrace{\lambda_j \sim \mathcal{C}^+(\mathbf{0}, \mathbf{1}),}_{\tau \sim \mathcal{C}^+(\mathbf{0}, \tau_0)}.$$

 Problem: non-zero slopes are unregularized, can result in nonidentification or weak identification.

# The prior

 Feature selection via the regularized Horseshoe prior [Piironen and Vehtari, 2017]

$$egin{aligned} eta_{j,s_n} &\sim \mathcal{N}(\mathbf{0}, au_{s_n}^2 ilde{\lambda}_{j,s_n}^2), \qquad ilde{\lambda}_{j,s_n}^2 &= rac{oldsymbol{c}^2 \lambda_{j,s_n}^2}{oldsymbol{c}^2 + oldsymbol{c}^2 \lambda_{j,s_n}^2}, \ \lambda_{j,s_n} &\sim \mathcal{C}^+(\mathbf{0},\mathbf{1}), \ oldsymbol{c}^2 &\sim \mathcal{IG}(rac{
u}{2},rac{
u}{2}oldsymbol{s}^2), \ au_{s_n} &\sim \mathcal{C}^+(\mathbf{0}, au_0). \end{aligned}$$

- Note: the subscripts  $s_n$  represent the site-specific variances for  $\beta_{i,s_n}$ .

#### Model capabilities

 Site-specific feature selection while information is borrowed across sites;



#### **Bayesian Feature Selection**

# Model capabilities

- The risk associated with missing HPV values are augmented and estimated as parameters;
- Automatically incorporating prediction uncertainty associated with missing HPV values;
- Can improve coverage by 20% according to simulation results.

# Model capabilities

Bayesian feature selection

- The Bayesian shrinkage priors provide uncertainty estimates for selected feature coefficients unlike their frequentist counterparts currently used;
- The regularized Horseshoe prior achieves reliable sparse inference.

Multiple steps unified within one hierarchical model implemented in Stan.

#### Features predictive of LN



#### Features predictive of HPV



#### The difference inclusion of HPV can make





LN with HPV in the model



# LN prediction Accuracy



0.81 <AUC< 0.84

The CV AUC obtained from random forest was 0.76.

**Bayesian Feature Selection** 

# HPV prediction Accuracy

0.85 <AUC< 0.91



# Work in progress and concluding remarks

Simulation study addressing

- To what extent the integrated inference can improve the results over a multi-step analysis?
- What are the problem settings (dimensionality, correlation structure, etc) that the proposed model works best within?

#### Main message

- Uncertainty quantification is important even when the main objective is prediction;
- The cost is the computation, especially as the dimensionality increases.

#### References



Betancourt, M. (2018).

Bayes sparse regression.

https://betanalpha.github.io/assets/case-studies/bayes-sparse-regression.html.



Carvalho, C. M., Polson, N. G., and Scott., J. G. (2009).

Handling sparsity via the horseshoe.

In Proceedings of the Twelth International Conference on Artificial Intelligence and Statistics.

Gillies, R. J., Kinahan, P. E., and Hricak, H. (2015).

Radiomics: Images are more than pictures, they are data. *Radiology*, 278(2).



Piironen, J. and Vehtari, A. (2017).

Sparsity information and regularization in the horseshoe and other shrinkage priors.

Electronic Journal of Statistics, 11(2):5018–5051.