

Data Generation

The dataset consists of 2,000 simulated images, each with a 16×16 grid of 256 pixels, split evenly into groups A and B. For images in group A, the central 8×8 region is subject to a β effect, which was adjusted visually to be noticeable yet minimal. Figure 1 displays an image without the β effect, Figure 2 shows the effect at a strength of 1.5, and Figure 3 at a strength of 2, with the latter chosen for subsequent analyses.

The β matrix values are zero except in the central region, and the `group_ind` vector classifies images into groups A (1) and B (0). Noise, ϵ_i , is added to each image, derived from a multivariate normal distribution with zero mean and a covariance structure based on an exponential correlation function with rate 1.

Question about how to generate exponential correlation matrix: for any two pixels, $\text{dist}(i, j) = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2}$. I found two ways to calculate the exponential correlation matrix online:

- $\text{cor}(i, j) = \exp(-\alpha \times \text{dist}(i, j))$, α is called rate;
- $\text{cor}(i, j) = \rho^{\text{dist}(i, j)}$, $\rho < 1$

I think we are aiming at the first one?

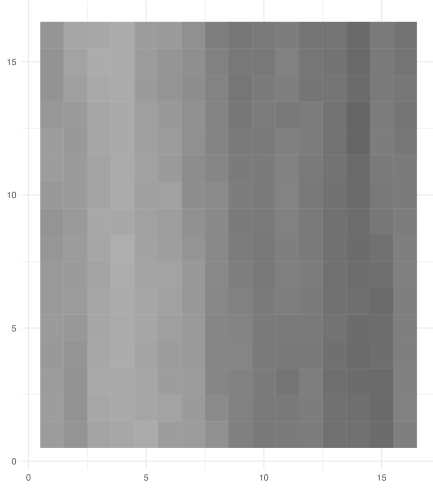


Figure 1: Example image without β effect

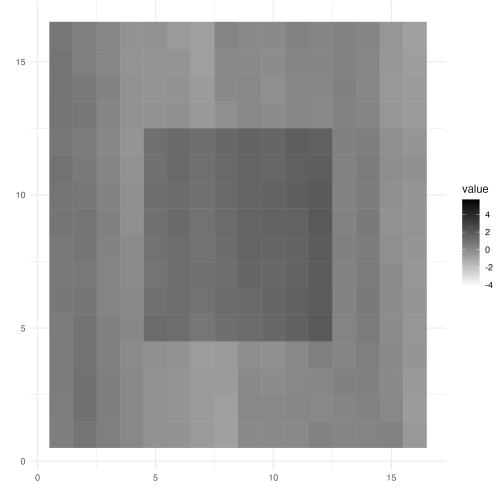


Figure 2: Example image with $\beta = 1.5$

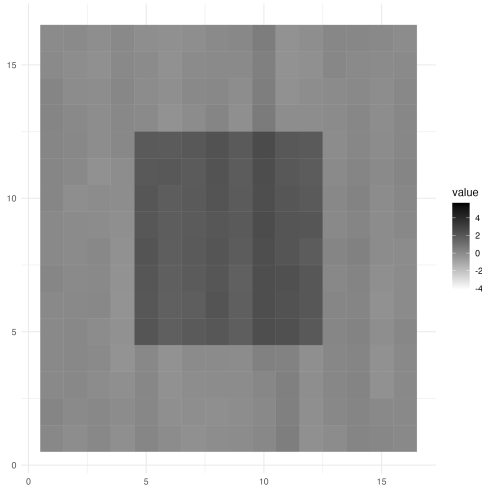


Figure 3: Example image with $\beta = 2$

VBM

In the VBM analysis, a Generalized Linear Model (GLM) was applied pixel-wise to assess group effects on pixel intensities across 100 iterations. For each iteration, the model generated effect size estimates and p-values for each pixel. These p-values were then corrected for multiple comparisons using the Bonferroni method. Figure ?? depicts the frequency of significant p-values in across pixels, with pixels showing significant β in all 100 iterations appearing in black, and those never showing significance in white.

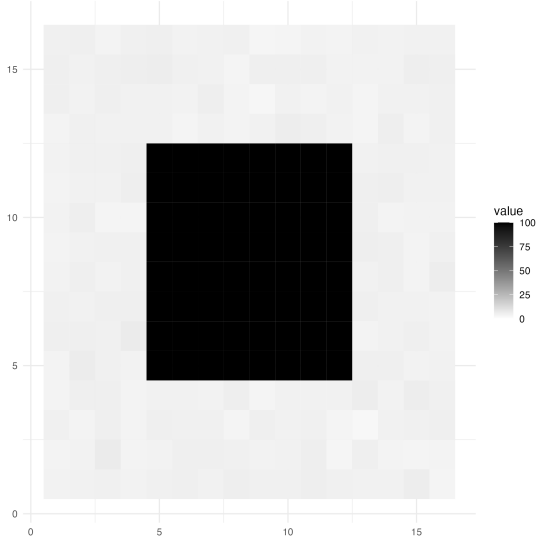


Figure 4: % of significant p-values across pixels in VBM analysis

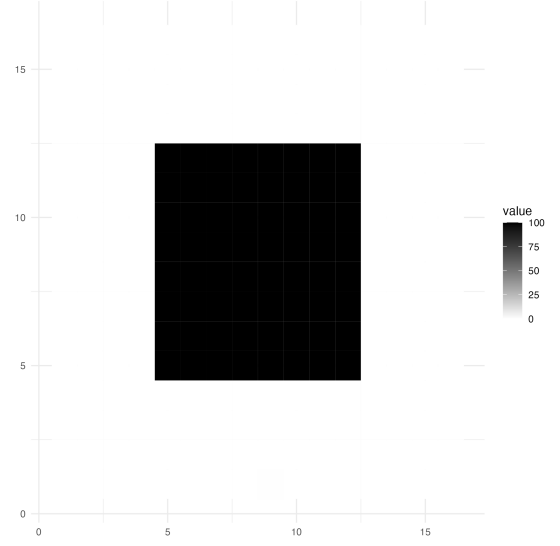


Figure 5: % of significant p-values after correction across pixels in VBM analysis

spVBM

The spVBM model is:

$$\begin{aligned}
 y_s^i &= \sum_{k=1}^K x_{s,k}^i \beta_{s,k}^{SVC} + \mathbf{Z}^i \mathbf{b}^i + \varepsilon_s^i \\
 \beta_{s,k}^{SVC} &= \beta_k + [\mathbf{E}\Gamma]_{s,k} \\
 \mathbf{b}^i &\sim \mathcal{N}(\mathbf{0}, G), \quad \varepsilon_i \sim \mathcal{N}(0, \sigma^2), \quad \Gamma_{,k} \sim \mathcal{N}(\mathbf{0}, \sigma_k^2 \mathbf{\Lambda}(\alpha_k))
 \end{aligned}$$

y_s^i denote the spatial outcome for subject i voxel s . \mathbf{Z} denote non-spatial subject-level covariates for non-spatial random effects.

In our simulated data, this could be simplified to $y_s^i = x_s^i \beta_s^{SVC} + (?)$. My question is, which term captures the exponential correlation structure in the model? G or Γ ?

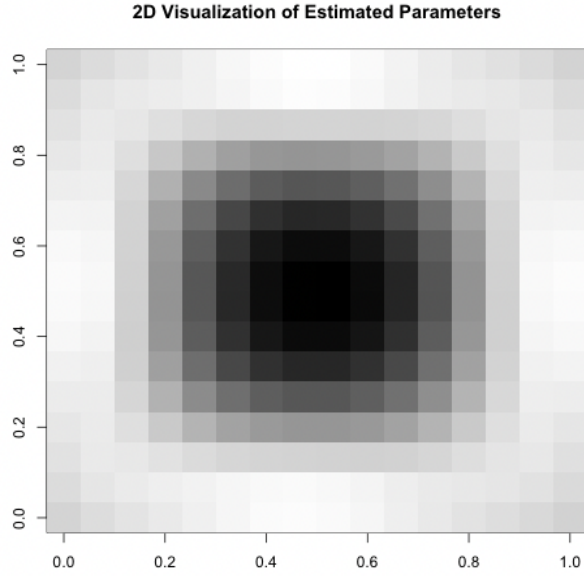


Figure 6: Estimated coefficients

LASSO

A LASSO model was employed to predict group assignments using pixel values from images. In each iteration, 80% of the data was used for training and the remaining 20% for testing. The optimal λ parameters, `lambda_min` and `lambda_1se`, were determined via cross-validation within the training group. The model's performance was assessed on the test group using accuracy and AUC metrics.

Initially, including all pixel values in the model led to perfect separation, indicating potential overfitting. To address this, the model construction began by incrementally adding one pixel from the image's edge and one from the center, evaluating if these additions achieved perfect accuracy. After integrating three pairs of pixels, totaling six pixels, the model achieved perfect separation.

Additionally, a permutation test was conducted to estimate p-values.

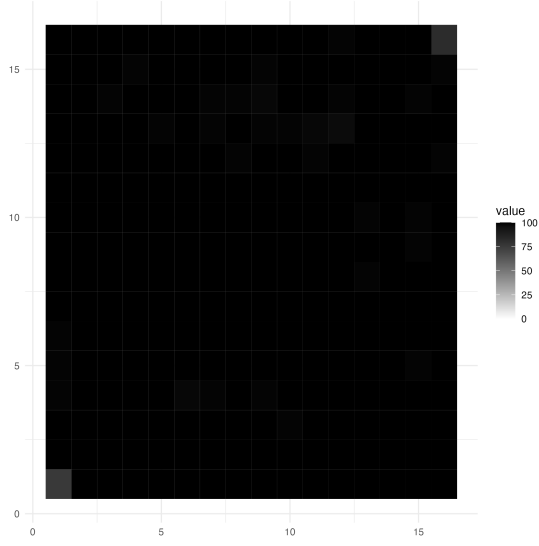


Figure 7: % of significant p-values across pixels in LASSO

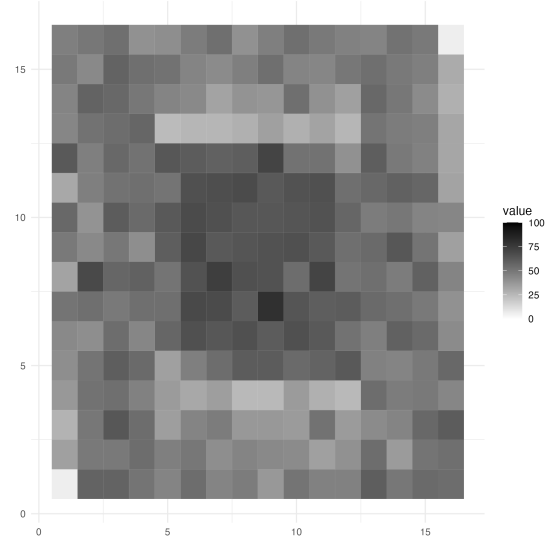


Figure 8: % of significant p-values after correction across pixels in LASSO

Frequency

An empirical correlation matrix was computed from the 2000×256 pixel matrix, followed by the extraction of eigenvectors and eigenvalues. The dataset X was then transformed using the eigenvectors corresponding to positive eigenvalues. A Lasso regression model was fitted on the transformed data to predict `group_ind`. The significance of the model coefficients was assessed using p-values obtained from 1000 permutation tests.