Algorithm 3: Hierarchical Clustering and Averaging Regression

1. Apply hierarchical clustering of the genes to yield the nested correlation structure. We define $\mathcal{G}_s = (\mathcal{G}_1^s, \ldots, \mathcal{G}_g^s, \ldots, \mathcal{G}_{G_s}^s)$ a group partition in G_s groups and $\mathbf{X}_{\mathcal{G}^s}^s = \left[\mathbf{X}_{\mathcal{G}_1^s}^s, \ldots, \mathbf{X}_{\mathcal{G}_{G_s}^s}^s \right]$ the concatenated matrix of variables for the partition $\mathcal{G}^s$.

2. for $s = 1, \ldots, S$ do

　　Create supergenes matrix $\tilde{\mathbf{X}}^s = \tilde{\mathbf{X}}_{\mathcal{G}_1^s}^s, \ldots, \tilde{\mathbf{X}}_{\mathcal{G}_{G_s}^s}^s$ by averaging the gene expressions at each cluster of the current group partition $\mathcal{G}^s$:

$$\tilde{x}_{ig}^s = \frac{1}{G_s} \sum_{g \in \mathcal{G}_s} \mathbf{x}_{i\mathcal{G}_g^s}^s \qquad \text{with } i = 1, \ldots, n$$

　　Fit Lasso, using the supergenes matrix $\tilde{\mathbf{X}}^s$ as input and retrieve the set of solution paths of the coefficients

end

3. Using cross-validation, find the optimal degree of shrinkage and level of the hierarchy.