**Input:** training set $TD$ with $G$ genes and $n$ samples

**Pre-processing step:** Rank-order all $G$ genes by applying Cox Proportional Hazards Regression to each individual gene. Let $x_1, x_2, \ldots, x_G$ be the ordered list of genes, sorted in descending order of log likelihood. Let $maxNvar$ denote the user-specified size of the BMA window (maximum 30).

**Parameters:** $nbest$ and $p$, where $p$ is the total number of genes to be processed such that $maxNvar < p \leq G$.

1. Initially, start with the $maxNvar$ top ranked genes ($x_1, x_2, \ldots, x_{maxNvar}$), and apply the traditional BMA algorithm for survival analysis (Volinsky et al., 1997). Let $toBeProcessed$ be an ordered list of genes with ranks $(maxNvar + 1)$ to $p$. Initially, $toBeProcessed \leftarrow (x_{maxNvar+1}, x_{32}, \ldots, x_p)$.

2. Repeat until all $p$ genes are processed
   a. Remove all genes $i$ with $Pr(b_i \neq 0 \mid TD) < 1\%$.
   b. Adaptive threshold step: If all genes have $Pr(b_i \neq 0 \mid TD) \geq 1\%$, determine the minimum $Pr(b_i \neq 0 \mid TD)$, $minProbne0$, among the $maxNvar$ genes in the current BMA window. Remove all genes with $Pr(b_i \neq 0 \mid TD) < (minProbne0 + 1)\%$.
   c. Let $removedGenes$ be the set of genes removed, and suppose $q$ genes are removed.
   d. Replace the $q$ removed genes with the $q$-next-up genes from $toBeProcessed$. Update $toBeProcessed \leftarrow toBeProcessed – q$-next-up.
   e. Apply the traditional BMA algorithm for survival analysis.

**Output:** selected models and their posterior probabilities, selected genes and their corresponding posterior probabilities ($Pr(b_i \neq 0 \mid TD)$), maximum-likelihood estimates of the regression parameters in each model.