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| **Variable** | **Description** |
| $$J$$ | Number of pools in screen |
| $$K$$ | Number of functional sequences |
| $$L$$ | Maximum length of functional sequence in genome segments |
| $$M$$ | Number of genome segments |
| $$N$$ | Number of sgRNAs |
| $$y$$ | Observed sgRNA counts (matrix of dimension $N×J$) |
| $$δ$$ | Functional sequence configuration (matrix of dimension $K×M$). Each row, $δ\_{k}$ specifies the placement (length and position) of functional sequence $k$. A specific placement is denoted $δ\_{k}[m,l]$, where $m$ is the genome segment containing the start of the functional sequence and $l$ is the length of the functional sequence. |
| $$π$$ | Probability a genome segment contains a specific functional sequence (matrix of dimension $K × M$) |
| $$α$$ | Hyperparameters for sorting probability distribution (vector of length $J$) |
| $$s$$ | sgRNA sorting probabilities (vector of length $N$) |
| $$r$$ | Number of genome segments that an sgRNA overlaps that contain a functional sequence (vector of length $N$) |
| $$p$$ | Probability genome segments contains any functional sequence (vector of length $M$) |
| $$l$$ | Length of a functional sequence |
| $$g(n)$$ | Mapping of sgRNAs to genome segments |