| Symbol | Description |
| --- | --- |
| $\boldsymbol{f}^{(t)}$ | Cumulative probabilities for each state at timestep $t$ |
| $\boldsymbol{f}^{(t)}$ | Tensor form of $\boldsymbol{f}^{(t)}$ |
| $\boldsymbol{O}^{(t)}$ | HMM Emission matrix for timestep $t$ |
| $\boldsymbol{\mathcal{O}}^{(t)}$ | Tensor form of $\boldsymbol{O}^{(t)}$ |
| $\widehat{\boldsymbol{\mathcal{O}}}^{(t)}$ | A pruned approximation of $\boldsymbol{\mathcal{O}}^{(t)}$ |
| $\boldsymbol{T}$ | The HMM transition matrix |
| $\boldsymbol{\mathcal{T}}$ | Tensor form of $\boldsymbol{T}$ |
| $\widehat{\boldsymbol{\mathcal{T}}}^{(t)}$ | A pruned approximation of $\boldsymbol{\mathcal{T}}$ at timestep $t$ |
| $T$ | The number of timesteps |
| $Y_{1:T}$ | Random variables representing the series of observations |
| $y_{1:T}$ | The true values of $Y_{1:T}$ |
| $X_{1:T}$ | Random variables representing the state of the HMM across time |
| $Z$ | Random variable representing the peptide |
| $z$ | True value of $Z$ |
| $s$ | The number of states of a fluorophore |
| $\Lambda$ | The number of fluorophores |
| $C$ | The number of colors of fluorophore |
| $\Lambda_c$ | The number of fluorophores of color $c$ |
| $\rho$ | Number of amino acids successfully removed by Edman degradation |
| $\bar{c}$ | Color of N-terminal amino acid |
| $\lambda_{\rho,c}$ | Number of amino acids which can accept a label of color $c$ when $\rho$ amino acids have been removed from the peptide |
| $\phi_c$ | Number of functioning fluorophores of color $c$ remaining for the peptide |
| $\alpha$ | Number of amino acids in the peptide (before sequencing) |
| $p_c$ | Fluorophore loss rate for color $c$ |
| $\boldsymbol{\mathcal{B}}^{(c)}$ | A factored component of $\boldsymbol{\mathcal{T}}$ representing loss of fluorophores of color $c$ |
| $\widehat{\boldsymbol{\mathcal{B}}}^{(t,c)}$ | A pruned approximation of $\widehat{\boldsymbol{\mathcal{B}}}^{(c)}$ at timestep $t$ |
| $e$ | Edman cycle failure rate |
| $\boldsymbol{\mathcal{E}}$ | A factored component of $\boldsymbol{\mathcal{T}}$ representing Edman degradation success and failure |
| $\widehat{\boldsymbol{\mathcal{E}}}^{(t)}$ | A pruned approximation of $\boldsymbol{\mathcal{E}}$ at timestep $t$ |
| $d$ | Peptide detachment rate |
| $\boldsymbol{\mathcal{D}}$ | A factored component of $\boldsymbol{\mathcal{T}}$ representing peptide detachment |
| $\widehat{\boldsymbol{\mathcal{D}}}^{(t)}$ | A pruned approximation of $\boldsymbol{\mathcal{D}}$ at timestep $t$ |
| $r$ | Number of values of $\boldsymbol{\mathcal{O}}$ kept during pruning |
| $r_c$ | Number of fluorophore counts of color $c$ kept during pruning |
| $r_c^{(t)}$ | $r_c$ at time $t$ |
| $\bar{r}$ | Number of amino acid counts kept during pruning |
| $\bar{r}^{(t)}$ | $\bar{r}$ at time $t$ |
| $h$ | The number of peptides selected by the kNN in the hybrid model |
| $\zeta_h$ | The set of peptides selected by the kNN in the hybrid model |