

State_array: has length equal to the number of ribosomes; describes which ribosome footprint the ribosome is translating at the moment; if ribosome is free, the respective number is one, if ribosome is at the beginning of the transcript, its state is two and if it is at the n^{th} position, its state is $n+1$. Note: this does not cause an issue, because if transcript has length n , beta array (see below) of that transcript is $n+1$ long, so protein is produced when the state is equal to the length of the corresponding beta array!

Location_array: has length equal to the number of ribosomes; describes which mRNA the ribosome is on, if the ribosome is free, the respective number is zero

Time_P_cell: cellular array, which has length equal to the number of types of mRNAs; the respective arrays store the times when a protein type was made from a given mRNA type

P_count_vec: has length equal to the number of protein types; the respective elements store the total number of proteins of the corresponding type

Betas: cellular array, which has length equal to the number of types of mRNAs; the respective arrays store the local elongation speed for each ribosome footprint on a given mRNA starting with initiation speed and hence have the length of the length of the mRNA plus one (because of initiation speed) Note: initiation rate should be reflected both in beta_array_cell and in temp!

Transition_array – as it is created when number of input arguments is 12: array, which has number of rows equal to the number of mRNAs and number of columns equal to the number of ribosomes; each row stores the current elongation speeds associated with the ribosomes that are on the respective mRNA, otherwise the element is zero

Transition_array – after merge and sum: 1D array, which has length of the number of ribosomes plus eight. The first element (created using an array called temp) corresponds to the total transition rate of the free ribosomes to any of the mRNAs, whereas the following elements (each element corresponding to one ribosome) correspond to the transition rate of a ribosome to the next position on the mRNA; if the ribosome is free, the element is zero. The seven last elements correspond to R transcription rate, E transcription rate, Q transcription rate, H transcription rate, degradation rate, nutrient transport rate and nutrient metabolism rate, respectively.

Temp: array, which has length equal to the number of mRNAs. Each element corresponds to the current initiation rate of the mRNAs taking into account that if the RBS site is occupied the current initiation rate is zero

Type_idx_array: array, which has length equal to the number of mRNAs. Each element denotes which type the corresponding mRNA belongs to.