
The following algorithm refers to `Translation.m` file

Located in `/wholecell115/WholeCell/src/+edu/+stanford/+covert/+cell/+sim/+process`

Algorithm consists of one preliminary step (Requirements calculation) and 3 consecutive steps (Elongation, Initiation, Termination). Energy is allocated in these steps as “first come first served”. For example it is possible that at one time step translation would not reach Initiation step, because there would be no more energy left. Of note, there are actively translating ribosomes at the very first.

```

    Calculate requirements ;                                /* line 383 */
    /* roughly calculate numbers based on maximum possible
       values. Lines 580-584                                */
    Calculate nInitiations;
    Calculate nElongations;
    Calculate nTerminations;
    Calculate GTP requirements as function nInitiations, nElongations,
    nTerminations ;                                       /* 1. 588 */
    Calculate other requirements (factors, water, etc);

    Initiation ;                                         /* line 740 */
    Calculate N=nInitiatingRibosomes as minimum of available ribosomes,
    factors, energy;
    Calculate resources, left for the next Translation step;
    /* Probs in the code means probabilities                */
    Randomly choose N particular mRNAs to bind to N ribosomes ;
    /* Probability is weighted by mRNA copy number */
    Update state;

    /* Actual translation starts from line 599              */
    Elongation ;                                         /* line 684 */
    Calculate N=nElongatingRibosomes as minimum of available active
    ribosomes, energy;
    Generate random order for ribosomes to be translated;
    foreach ElongatingRibosome do
        if GTP, EF available then
            Extract portion of sequence to be translated ; /* line 705 */
            if AA-tRNA available then
                Associate AA-tRNA ;                       /* line 772 */
                Release free tRNA;
                Update states;

    Termination ;                                       /* line 814 */
    Randomly permute the order of fully elongated ribosomes;
    foreach elongated ribosome do
        if Energy, termination factors are available then
            Release peptide, mRNA, ribosome subunits;
            Update states;

```

Algorithm 1: Translation algorithm in WholeCell model. Line numbers correspond to Translation.m (1/4/2010)