Codon documentation – Business logic layer   Sungjae Song

In middle folder:

- codoncal.py : API which calculate codon usage, it includes percentage of each codons in the sequence and relative ratio of each codons in amino acid.

> codon_aa: dictionary, which contain all codons and its counterpart amino acids, "Z" is stop codon

> upper(cds): change lowercased written – coding sequences into uppercase.

> rem_vague(cds): sometimes there is ambiguous nucleotides(such as N) are appeared on the sequence, and it cannot be translate into amino acid sequence, so needed to remove it when the calculation is going on.

> count_codon(cds): count how many each codons are appeared on the sequence.

> translate(cds,codon_aa): translate the codons into amino acid sequence, by using codon_aa dictionary

> count_perce_codons(cds): calculate percentage of each codons in sequences

> count_relev_perce_codons(cds): calculate relative ratio of each codons in each amino acids.

- res.py: API which find the location of restriction enzyme site

> enzymes: dictionary, it contains name of the enzyme as key and its restriction enzyme cutting sequence as value

> giveme_res(sequence): find all restriction enzyme site in given sequences

> single_res(enzyme,sequence): find all restriction enzyme site of selected enzyme. The name of enzyme should be typed in 'enzyme'

> custom_search_res(res_seq,sequence): find all restriction enzyme site by searching enzyme cutting region of which user typed. In other words, finding restriction enzyme site with custom restriction enzyme cutting sequence

-goodorbad.py: API which judge whether the given enzyme is good or bad

good_bad(): it will show the restriction enzyme is good or bad for the sequence

- precal.py: precalculation of codon usage in human chromosome 3

chr3precal_per(): precalculation of percentage in human chromosome3

chr3precal_rel():pre calulation of relative ratio in amino acids in human chromosome3

- chromosome_codon_usage.csv : csv file where precalculation result is stored.