Detection of meaningful cancerous mutations should be helpful both for diagnosis and for developing novel therapies. Regions in the coding sequence that are conserved at the synonymous level encode additional regulatory elements. We want to show that those regions tend to include a significant number of cancerous mutations.

**Introduction**

Regions in the coding sequence that are conserved at the synonymous level encode additional regulatory elements. We want to show that those regions tend to include a significant number of cancerous mutations.

**Methods**

Sum up the total number of repetitions (number of patients) of all the mutations which appear in the conserved regions. Create a null model by changing the location of each mutation to the same codon but in a different position in the ORF. From the null model, we can get the Distribution of the total number of repetitions for random positions.

**Results**

Recurrent mutations tend to appear in these regulatory regions while non-recurrent mutations do not. Both in silent and non-silent mutations.

**Conclusions**

The results suggest that if a mutation appears in such conserved region then it is a driver mutation (has a selective advantage). Evolutionary conservation can be used as an important feature for evaluating the effect of cancerous mutations on the fitness of the cancer cell. Many non-silent cancerous mutations are selected for due to their effect on gene expression regulation and not due to their effect on the protein structure.