CRAVAT

CRAVAT: Cancer-related Annotation of Variants Toolkit

A web application for cancer mutation analysis – the tool accepts mutations as input and maps them onto genome.

Cancer exome sequencing projects identify a large number of tumor-derived mutations and increasingly rely on computational tools. To begin to address this need, our team designed the CHASM method to prioritize missense mutations, which is now used in many large-scale exome sequencing projects. We have also produced several tools to utilize protein structure for mutation analysis. Our tools have contributed to studies of many cancer types, with our direct participation. However, not every cancer researcher has access to collaborators who are bioinformatics specialists. We have now created web applications for cancer mutation analysis, which are accessible to researchers whose expertise is not primarily computational and who lack strong bioinformatics collaborators. The Cancer-related Annotation of Variants Toolkit (CRAVAT) accepts user input of millions of mutations and provides mapping of mutations onto genomic features, annotations, functional predictions of missense mutations, and gene scores.

Here is a brief video that highlights the capabilities of CRAVAT.

Learn more about the utility and value of this open source bioinformatics application at CRAVAT Introduction Video - Cancer Related Analysis of Variants

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