

SeqAnt: Next Generation Sequencing Annotation web Application

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Next generation sequencing technologies has made detecting DNA variants both cost efficient and fast. Researchers and clinical geneticists can now possibly perform single experiments to identify millions of variant sites. SeqAnt, open source web annotation software was developed to efficiently annotate the large datasets generated from second generation sequencing platforms that are not easily characterized using publicly available websites. I had worked on upgrading features of SeqAnt to allow for DNA variant annotation of more species and the inclusion of more conservation score tracks to enhance variant characterization. The ongoing upgrades on SeqAnt is aimed at creating a tool that could as well be adapted to analyzing and utilizing high throughput population data, such as those from the 1000 genomes project.