MGvizCE: Clinical Exome QC and Analytics

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NGS facilities dedicated for clinical genomics need high QC standards, and they need continuously keeping track of their experiments and their metrics. As part of the Medical Genomics Visualization toolset (MGviz) we have developed an interactive software suit with R-Shiny and Python (Bokeh, crossfilter, flask and ReportLab) for automatic reports of QC for the whole NGS experiments in clinical diagnostics labs. The tool allows comparison of the current experiment with historic data to see the performance of the sequencer, checking different metrics for coverage and variations, warning for large copy number regions. In addition it remembers decisions over annotations, helps in variant prioritization, segregation and finding compound heterozygotes and make automatic historical reports of pathogenic variants informed by the lab.









MGviz is a web and CLI tool very useful for QC and analytics for exome and amplicon NGS. Here we have shown only the QC and visualization tools.

Code will be released on July at github. https://github.com/MGviz-soft

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