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**Title**
CNViz: an R/Shiny Application For Interactive Copy Number Variant Visualization in Cancer

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**Introduction**: Copy number variants (CNVs) include deletion, duplication or amplification events that range in size from smaller than a single-gene or exon, to the size of a full chromosome. These changes can affect gene expression levels and are thus implicated in disease, including cancer. Although a variety of tools and methodologies exist to estimate the copy number profile for data from massively parallel sequencing (MPS, also referred to as next-generation sequencing or NGS), it can be difficult to appreciate such complex information in a list format or as a static image. Static scatterplots and diagrams allow for visualization of large events on the chromosome-level, but gene-level or sub-gene-level information is not easily accessible.

**Methods**: CNViz is a freely accessible R/Bioconductor package that launches an interactive R/Shiny visualization tool to facilitate review of copy number data. As inputs, it requires genomic coordinates and corresponding copy number ratios for probe, gene and/or segment-level data. If supplied, loss of heterozygosity (LOH), focal variant data (single nucleotide variants [SNVs] and small insertions and deletions), and metadata (e.g. specimen purity and ploidy) can also be incorporated into the visualization. CNViz includes aggregated data from The Cancer Genome Atlas (TCGA) 2018 Pan-Cancer Atlas studies so findings can be correlated with those seen in a variety of common cancer diagnoses.

**Results**: A case of glioblastoma multiforme is reviewed using CNViz. The ability to visualize chromosome events, such as arm gains and LOH, is displayed. Focal variants and copy number variations are illuminated through colored visualization, and interactive exploration of gene and probe data is demonstrated. TCGA Pan-Cancer Atlas 2018 data is explored to compare CNV findings to publicly available glioblastoma multiforme cases.

**Conclusions**: The CNViz R package is an easy-to-use tool encouraging visualization and exploration of copy number variation. CNViz can be used in a clinical setting as well as for research to study patterns in human cancers more broadly. The intuitive interface allows
visualization of the copy number profile of a specimen, dynamic multi-level resolution to explore gene and probe-level copy number changes, and integration of LOH and focal variant data. CNViz is available for download as an R package via Bioconductor. An interactive example of the application is available at rebeccagreenblatt.shinyapps.io/cnviz_example.