

Genome analysis

svpluscnv: analysis and visualization of complex structural variation data

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Abstract

Motivation: Despite widespread prevalence of somatic structural variations (SVs) across most tumor types, understanding of their molecular implications often remains poor. SVs are extremely heterogeneous in size and complexity, hindering the interpretation of their pathogenic role. Tools integrating large SV datasets across platforms are required to fully characterize the cancer's somatic landscape.

Results: *svpluscnv* R package is a *swiss army knife* for the integration and interpretation of orthogonal datasets including copy number variant segmentation profiles and sequencing-based structural variant calls. The package implements analysis and visualization tools to evaluate chromosomal instability and ploidy, identify genes harboring recurrent SVs and detects complex rearrangements such as chromothripsis and chromoplexia. Further, it allows systematic identification of *hot-spot* shattered genomic regions, showing reproducibility across alternative detection methods and datasets.

Availability and implementation: <https://github.com/ccbiolab/svpluscnv>.

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Supplementary information: [Supplementary data](#) are available at *Bioinformatics* online.

1 Introduction

Somatic structural variations (SVs) are a fundamental contributor to cancer genetics and pathogenesis (Futreal *et al.*, 2004). Historically, copy number variants (CNVs) have been instrumental in cancer diagnosis and classification. Genome-wide profiling via genotyping or comparative genomic hybridization (CGH) arrays coupled with tools such as GISTIC (Mermel *et al.*, 2011) have facilitated identification of oncogenic events. However, the surge of available large whole genome sequencing (WGS) cancer datasets is expanding our understanding of the role of SVs (Consortium, 2020; Grobner *et al.*, 2018; Ma *et al.*, 2018) and has revealed widespread prevalence of complex catastrophic events such as chromothripsis and chromoplexia (Cortes-Ciriano *et al.*, 2020).

Recently, we integrated CNVs from genotyping arrays with structural variant calls (SVCs) from WGS in a neuroblastoma cohort, showing that orthogonal data types allowed identification of novel oncogenic alterations and revealed insights about the pathogenic role of chromothripsis (Lopez *et al.*, 2020). Here, we implement the methodological framework into an R package

incorporating multiple functionalities to integrate orthogonal data types and characterize SVs in large cancer datasets.

2 Materials and methods

The *svpluscnv* R package operates with two input data types: (i) CNV: segmentation profiles including logR (E.g. log₂ of the ratio of the signal between paired samples; e.g. tumor/normal). CNVs derive from arrays (SNP, CGH) as well as sequencing read-depth data and provide genome-wide gain/loss dosage information. (ii) SVC: derived from WGS discordantly aligned reads. A plethora of available algorithms use different approaches to identify SVC (reviewed in Kosugi *et al.*, 2019). Variant classes include: duplication (DUP), deletion (DEL), inversion (INV), insertion (INS), translocation (TRA) and break-end (BND) for undefined SVCs.

2.1 Integrated analyses of CNV and SV datasets

Aneuploidy and CNV visualization: (i) '*cnv.freq.plot*' maps segments with copy number logR $\neq 0$ across samples and plots a genome

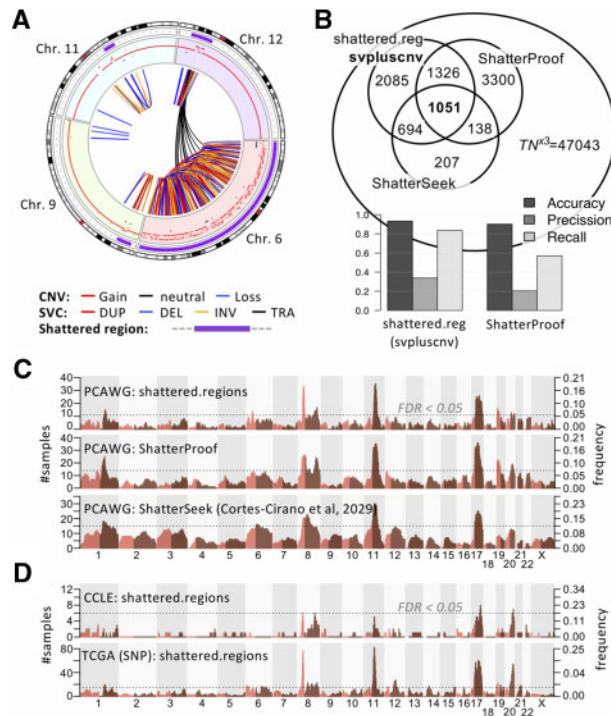


Fig 1. Identification of shattered chromosome regions. (A) Circos plot representing a breast cancer sample (BRCA-UK: SA541850) shows shattered regions at 6, 9, 11 and 12 Chromosomes (purple band), CNVs (outer) and SVCs (inner) tracks. (B) Venn diagram representing the overlap of shattered chromosomes detected by three different methods across all PCAWG samples (top) and prediction performance (bottom); (C, D) Genome wide shattered region frequency maps and their FDR < 0.05 threshold (Supplementary Fig. S4) of (C) PCAWG breast cancer samples derived from *shattered.regions* (top), *ShatterProof* (middle) and *ShatterSeek* (bottom); (D) *shattered.regions* identified in breast cancer cell lines (top) and TCGA samples (bottom)

wide map of gain/loss frequencies (Supplementary Fig. S1); (ii) ‘*chr.arm.cnv*’ retrieves chromosome arm median CNV logR values.

Chromosomal instability measurements: (i) ‘*percent.genome.changed*’ measures the percentage of the genome’s CN with logR \neq 0; (ii) ‘*cnv.breaks*’ identifies CNV breakpoints based on fold change threshold of CN between contiguous segments and (iii) ‘*svc.breaks*’ reports per sample SVC breakpoints. Finally, ‘*match.breaks*’ identifies colocalizing breakpoints between CNV and SVC for a set of common samples.

Gene annotation functionalities: (i) ‘*gene.cnv*’ transforms segmentation data into a gene-level CN matrix from which amplifications and deletions can be queried. (ii) ‘*cnv.break.annot*’ and ‘*svc.break.annot*’ provides genomic feature annotation tools for CNV and SVC breakpoints such as overlapping genes and their upstream regions (Supplementary Fig. S2). Finally, ‘*sv.model.view*’ and ‘*gene.track.view*’ display genomic track visualizations overlaying CNV and SVC for defined regions (Supplementary Fig. S2).

2.2 Chromosome shattering and hot-spot analyses

‘*shattered.regions*’ combines CNVs and SVCs to identify complex rearrangements. The algorithm is highly parametrizable and follows two major steps: (i) identification of High Breakpoint Density (HBD) genomic bins: breakpoints are mapped into a default 10 Mb sliding genomic windows calculated every 2 Mb, and (ii) shattered regions are defined by collapsing contiguous HBDs. Next, further testing for true likely catastrophic events uses information about interleaved SVCs, links between distant regions and the dispersion of breakpoints within regions (Supplementary Date). A simplified ‘*shattered.regions.cnv*’ algorithm, identifies catastrophic events using CNV segmentation data only. It follows same approach as

shattered.regions, using only parameters derived from CNV. A ‘*circ.chromo.plot*’ function wraps *circize* (Gu et al., 2014) functionalities for circos plotting zooming into shattered regions (Fig. 1A).

‘*shattered.map.plot*’ generates a genome wide map of regions with chromosome shattering and their frequencies (Fig. 1C and D). Using a permutation test ‘*freq.p.test*’ assigns corrected *P*-values to observed frequencies defining hot-spots regions above significance threshold; such regions are deemed under selection pressure for chromosome shattering.

3 Results

3.1 Integrated SV analysis of cancer datasets

In order to test *svpluscnv* tools, we compared the results obtained from analyzing different breast cancer cell line and primary tumor datasets including: 59 CCLC cell lines (Ghandi et al., 2019), 1088 primary tumors from TCGA and 198 breast adenocarcinomas from PCAWG (Consortium, 2020). The three datasets presented similar CNV gain/loss frequency profiles (Supplementary Fig. S1). We mapped breakpoints to known genes and ranked altered genes, again showing concordance across the three datasets (Supplementary Fig. S2A–C); 35 of 59 breast lines had orthogonal data from SNP (CNV) and WGS (SVC) profiles. We observed complete overlap of CNV and SVC breakpoints in the most frequently altered gene and fragile site, *FHIT* (Supplementary Fig. S2D). Overall, 30.2–28.3% of all breakpoints colocalized across CNV and SVC data types (Supplementary Fig. S3).

3.2 Analysis of shattered regions

In order to test the *shattered.regions* algorithm with other available tools, we evaluated 2658 human cancer whole genomes, previously analyzed with the algorithm *ShatterSeek* and manually curated (Cortes-Ciriano et al., 2020). In addition, we obtained predictions from *ShatterProof* (Govind et al., 2014) for the same set of samples using default parameters. The three sets of predictions significantly overlapped (*P*-value < 2.2e-16, Fig. 1B, Supplementary Data). We then used the curated set (*ShatterSeek*) as the gold standard to test for the precision/recall performance: *shattered.regions* achieved superior results (*pre* = 0.34; *rec* = 0.83) compared to *ShatterProof* (*pre* = 0.20; *rec* = 0.57) although the later allows additional input data types (i.e. Loss of Heterozygosity) not included here (Fig. 1B).

svpluscnv introduces a novel tool to identify recurrently shattered regions that could be under selection pressure in cancer histotypes. We evaluated PCAWG breast dataset shattered regions calculated using alternative algorithms (Fig. 1C); the three methods returned a strongly similar landscape of genome-wide frequencies (Pearson’s correlation *P*-value < 2.2 × 10⁻¹⁶, Supplementary Fig. S5A–C); The same landscape was reproduced when tested across two additional datasets including breast cancer derived cell lines (CCLC) and primary tumors from TCGA (based on CNV data only) (Fig. 1D, Supplementary Fig. S5D). Recurrently shattered regions (FDR < 0.05) were identified in chr8p11, chr8q24 (*MYC* locus), chr11q13 (*CCND1* locus), chr17q and chr20q in all three datasets; highlighting their reproducibility and likely biological relevance (Fig. 1C and D, Supplementary Fig. S4).

4 Conclusion

svpluscnv aims to become instrumental in the study of SVs in cancer genomics, enabling the identification of recurrent complex rearrangements that may pinpoint disease driver events. This toolset allows the research community to easily perform complex analysis of high throughput SV profiling data and will support extensions to further integrate analyses of other types of omics data.

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Conflict of Interest: none declared.

Data Availability

No new data were generated or analysed in support of this research.

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