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Genome analysis

SnoopCGH: software for visualizing comparative genomic hybridization data

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ABSTRACT

Summary: Array-based comparative genomic hybridization (CGH) technology is used to discover and validate genomic structural variation, including copy number variants, insertions, deletions and other structural variants (SVs). The visualization and summarization of the array CGH data outputs, potentially across many samples, is an important process in the identification and analysis of SVs. We have developed a software tool for SV analysis using data from array CGH technologies, which is also amenable to short-read sequence data.

Availability and implementation: SnoopCGH is written in java and is available from http://snoopcgh.sourceforge.net/

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2 FEATURES OF SNOOPCGH

SnoopCGH is a java-based standalone application that inputs CGH data in tab-, space- or comma-delimited format, containing columns with: chromosome number, probe name, probe starting and end positions, and a series of log intensity values corresponding to one or more comparisons or samples. It is possible to load more than one data file. The use of multiple window layers facilitates the visualization of subsets of data, with the ability to zoom in and out of regions of interest. SV breakpoint analysis methods are implemented and enable the rapid visualization and dissection of putative SV regions. In particular, data are smoothed using an algorithm based on Haar wavelets (Ben-Yaacov and Eldar, 2008), and islands of potential SVs are estimated using a Smith–Waterman algorithm (Price et al., 2005). The Haar wavelet approach has two smoothing parameters, namely start and end levels, that influence the sensitivity to the size of segments and trends, respectively. The default settings in SnoopCGH are based on suggested values in Ben-Yaacov and Eldar (2008). The breakpoint algorithms estimate levels of statistical significance and robustness of putative SVs using permutations. Prior to their application we may remove outliers to improve robustness using thresholds based on median absolute deviation statistics. The quantification of putative SVs leads to an ability to rank the regions of interest. We have also implemented a rank-based algorithm that considers differences in SVs between (groups of) samples (Laframboise et al., 2009). This extension may assist those working on association studies or multiple population studies considering differences in genetic variation. The strength of SnoopCGH is its ability to interface with downloadable annotation files (e.g. emb and gff formats) from genomic browsers, that include

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the annotation navigator window for the PfMDR1 gene located in the subregion; (pink) that is both statistically significant (\(P < 0.0001\)) and > 90% robust in a sensitivity analysis. Annotation tracks are presented at the bottom, and (B) shows the Haar wavelet smoothed values for part of the PfMDR1 gene.

![Image of SnoopCGH analysis](image)

Fig. 1. (A) The log2 intensities of the five strains for \(\sim 600\) kb of chromosome 5, with a separate window highlighting the IT data (blue), and a subregion (pink) that is both statistically significant (\(P < 0.0001\)) and > 90% robust in a sensitivity analysis. Annotation tracks are presented at the bottom, and (B) shows the Haar wavelet smoothed values for part of the PfMDR1 gene.

It is also possible to read in other useful information, such as the results from breakpoint analyses run externally.

3 APPLICATION TO A PARASITE CGH ARRAY

*Plasmodium falciparum* (Pf) malaria has an enormous morbidity and mortality burden in sub-Saharan Africa. The Pf genome is AT rich (80%), and contains some CNVs associated with drug resistance and erythrocyte invasion (Nair et al., 2008). The Pf CGH array was designed at the Wellcome Trust Sanger Institute and consists of \(\sim 2\) million 25 bp probes (many overlapping, but all mapping uniquely). It is being applied in an ongoing SV discovery study involving five Pf laboratory strains: 3D7 (the reference, African), DD2 (Indonesian), HB3 (Honduran), IT (South American or South East Asian) and PFClin (Ghanaian). We demonstrate the usefulness of SnoopCGH using screenshots of chromosome 5 data. Figure 1A shows the log2 intensities in a \(\sim 600\) kb region normalized using an average of all five strains. A separate window layer highlights a region of the IT genome that could contain increased copy number variation. This region includes coding sequence (CDS). Gene information (e.g. name, ontology, GC content) uploaded into SnoopCGH (Fig. 1B) indicates that this region contains the multi-drug resistance CNV (PfMDR1); (Price et al., 2004). Applying the Smith-Waterman algorithm to the IT data, highlighted (only) the region containing PfMDR1 as being both highly statistically significant (\(P < 0.0001\)) and robust to a sensitivity analysis (Fig. 1A). It is possible to change the analysis settings and methods, and move the resulting window layers across the genome. Changing the resolution of the frame also facilitates rapid dissection of data and erythrocyte invasion (Nair et al., 2008). The Pf genome is AT rich (80%), and contains some CNVs associated with drug resistance and erythrocyte invasion (Nair et al., 2008). The Pf CGH array was designed at the Wellcome Trust Sanger Institute and consists of \(\sim 2\) million 25 bp probes (many overlapping, but all mapping uniquely). It is being applied in an ongoing SV discovery study involving five Pf laboratory strains: 3D7 (the reference, African), DD2 (Indonesian), HB3 (Honduran), IT (South American or South East Asian) and PFClin (Ghanaian). We demonstrate the usefulness of SnoopCGH using screenshots of chromosome 5 data. Figure 1A shows the log2 intensities in a \(\sim 600\) kb region normalized using an average of all five strains. A separate window layer highlights a region of the IT genome that could contain increased copy number variation. This region includes coding sequence (CDS). Gene information (e.g. name, ontology, GC content) uploaded into SnoopCGH (Fig. 1B) indicates that this region contains the multi-drug resistance CNV (PfMDR1); (Price et al., 2004). Applying the Smith-Waterman algorithm to the IT data, highlighted (only) the region containing PfMDR1 as being both highly statistically significant (\(P < 0.0001\)) and robust to a sensitivity analysis (Fig. 1A). It is possible to change the analysis settings and methods, and move the resulting window layers across the genome. Changing the resolution of the frame also facilitates rapid dissection of data and analysis results. For example, Figure 1C presents the Haar wavelet smooth for the intensities from a subset of 23 probes for the region containing PfMDR1 as being both highly statistically significant (\(P < 0.0001\)) and robust to a sensitivity analysis (Fig. 1A). It is possible to change the analysis settings and methods, and move the resulting window layers across the genome. Changing the resolution of the frame also facilitates rapid dissection of data and analysis results. For example, Figure 1C presents the Haar wavelet smooth for the intensities from a subset of 23 probes for the region containing PfMDR1 as being both highly statistically significant (\(P < 0.0001\)) and robust to a sensitivity analysis (Fig. 1A).

4 DISCUSSION

SnoopCGH enables the visual assessment of genomes for SVs, with an estimation of their locations and statistical significance, as well as the ability to cross-check with external information (e.g. sequence annotation). Although we have implemented several fast breakpoint analytical methods, more sophisticated and computationally expensive approaches are being developed. These may be incorporated into a SnoopCGH analysis by either reading in the results from file or incorporating the method itself into our flexible software architecture. Ongoing work involves implementing new breakpoint detection methods, and incorporating tools to highlight the concordance of results from alternative SV detection methods. SVs may be detected using data from new sequencing technologies by considering differences in nucleotide coverage between target and reference genomes. It is possible to use SnoopCGH on such data, where (log transformed) ratios of normalized coverage (within or between samples) substitute for log ratios of normalized fluorescence intensities. However, sufficient consideration should be given to issues in the preprocessing steps, such as the uniqueness of read mappings, sequencing and assembly errors, and normalization accounting for GC content. In conclusion, SnoopCGH is a powerful visualization and analysis tool for those analyzing CGH data and discovering SVs genomewide, and has potential utility for those using new sequencing technologies for the same purpose.

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**REFERENCES**


