SVclone: inferring structural variant cancer cell fraction

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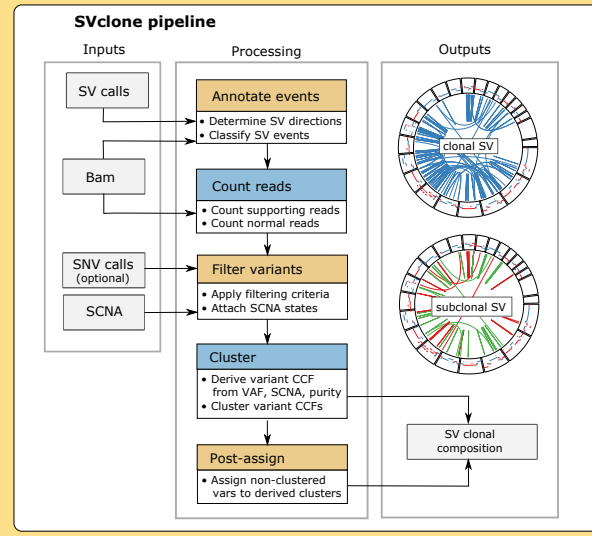
Motivation

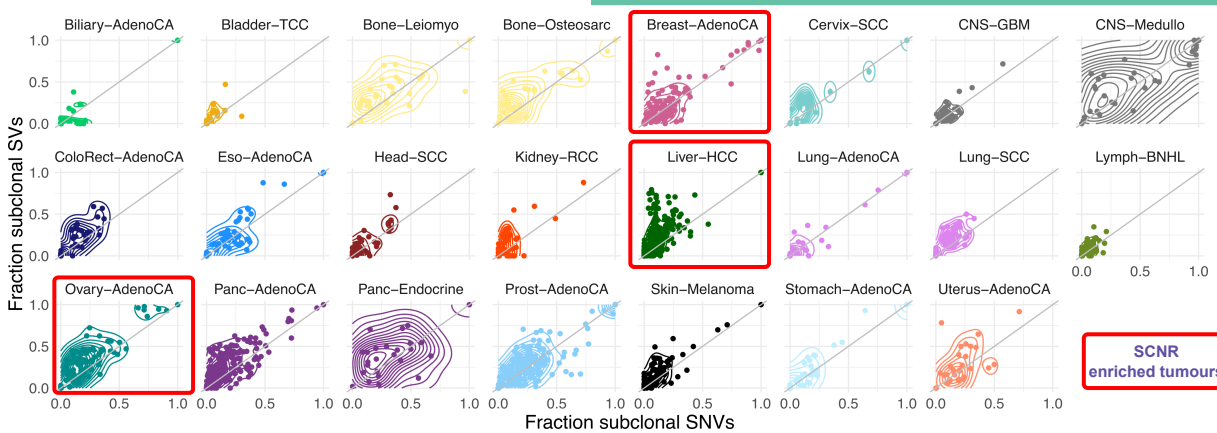
Structural variants are prominent drivers of tumourigenesis across many different cancer types, such as prostate and ovarian cancers. Methods exist that model the clonal architecture of tumours using SNVs or SCNAs, however, none exist that incorporate SV breakpoints. We present SVclone, a method for inferring the subclonal make up of tumour samples using SV calls obtained from whole-genome sequencing data.

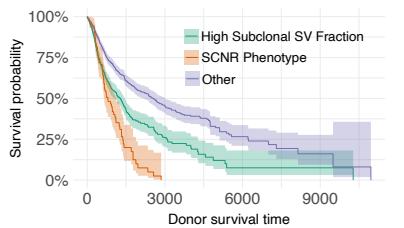
Method overview



Pan-cancer analysis

- We applied SVclone to 2,788 whole tumour genomes from the ICGC/TCGA pan-cancer analysis of whole genomes (PCAWG) project
- We found a sample subset with an enrichment of subclonal copy-number neutral rearrangements (SCNR)
- SCNR phenotype samples had decreased overall survival

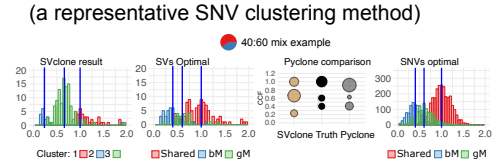


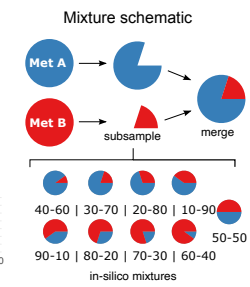


Survival curve comparing subclonal neutral rearrangement (SCNR), SV-enriched and all other PCAWG samples

Algorithm validation

- We subsampled and merged clonal tumours from the same patient in known proportions
- SVclone found the correct number of clusters and their approximate proportions using SVs
- Results were comparable to Pyclone (a representative SNV clustering method)





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nectar

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https://doi.org/10.1101/172486 (preprint)
https://github.com/mcmero/svclone
(scan for preprint link)

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