

## Supplementary Materials

**Supplementary Table S1.** Comparison of copy number and subclonal architecture of difference inference methods

Property	Sclust	SVclone	PhyloWGS	FastClone	PyClone	DPclust	PhylogicNDT	CITUP	SciClone	CLiP	CloneFinder	TrAp
Performs own copy-number segmentation	Y	N	N	N	N	N	N	N	N	N	N	N
Uses rearrangement breakpoints in segmentations	Y	Y	N	N	N	N	N	N	N	N	N	N
Calls absolute clonal copy numbers	Y	Y	N	N	N	N	N	N	N	N	N	N
Calls subclonal copy numbers	Y	Y	N	N	N	N	N	N	N	N	N	N
Clusters copy number alteration	Y	Y	Y	N	N	N	N	N	N	N	N	N
Deals with sample(s)	1	1	≥1	1	≥1	≥1	≥1	≥1	≥1	1	≥1	≥1
Reconstructs phylogenetic trees	N	N	Y	Y	N	N	Y	Y	N	N	Y	Y
Allows subclonal copy numbers for clustering	Y	Y	Y	Y	Y	Y	N	N	Y	N	N	N
Programming language	C++	R Python	Python Tex JavaScript, C++ HTML CSS	Python	Python	R	HTML Python	C++ Python	R	R Python	Python	Java

"Y" denotes the method performs the corresponding function.

**Sclust**, Software: [rj.run/downloads/Sclust.tgz](https://github.com/rjrun/downloads/Sclust.tgz), Cun Y, Yang TP, Achter V, Lang U, Peifer M. 2018. Copy-number analysis and inference of subclonal populations in cancer genomes using Sclust. Nat Protoc, 13(6): 1488-1501.

**SVclone**, Software: <https://github.com/mcmerno/Svclone>, Cmero et al, 2020: Inferring structural variant cancer cell fraction. Nature Communications, 11(1): 730.

**PhyloWGS**, Software: <https://github.com/morrislab/phyloWGS>, Deshwar AG, Vembu S, Yung CK, Jang GH, Stein L, Morris Q. 2015. PhyloWGS: Reconstructing subclonal composition and evolution from whole-genome sequencing of tumors. Genome Biology, 16(1): 35.

**FastClone**, Software: [https://github.com/GuanLab/FastClone\\_Guanlab](https://github.com/GuanLab/FastClone_Guanlab), Xiao Y, Wang X, Zhang H, Ulintz PJ, Li H, Guan Y. 2020. FastClone is a probabilistic tool for deconvoluting tumor heterogeneity in bulk-sequencing samples. Nature Communications, 11(1): 4469.

**PyClone**, Software: <https://shahlab.ca/projects/pyclone/>, Roth et al 2014. PyClone: statistical inference of clonal population structure in cancer. Nature Methods, 11(4): 396-398.

**Dpclust**, Software: <https://github.com/Wedge-Oxford/dpclust>, Nik-Zainal, et al, 2012: The Life History of 21 Breast Cancers. Cell, 149(5): 994-1007.

**PhylogicNDT**, Software: <https://github.com/broadinstitute/PhylogicNDT>, Gruber et al, 2019: Growth dynamics in naturally progressing chronic lymphocytic leukaemia. Nature, 570(7762): 474-479.

**CITUP**, Software: <http://sourceforge.net/projects/citup/>, Malikic S, Mcpherson AW, Donmez N, Sahinalp CS. 2015. Clonality inference in multiple tumor samples using phylogeny. Bioinformatics, 31(9): 1349-1356.

**SciClone**, Software: <https://github.com/genome/scicloner>, Miller et al, 2014. SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLOS Computational Biology, 10(8): e1003665.

**CLiP**, Software: <https://github.com/wwylab/CLiP>

**CloneFinder (2018, 11c, fast)** : <https://github.com/gstecher/CloneFinderAPI>, Miura S, Gomez K, Murillo O, Huuki LA, Vu T, Buturla T, Kumar S. 2018. Predicting clone genotypes from tumor bulk sequencing of multiple samples. Bioinformatics, 34(23): 4017-4026.

**TrAp**: <https://tinyheero.github.io/2015/08/26/TrAp.html>, Strino F, Parisi F, Micsinai M, Kluger Y. 2013. TrAp: a tree approach for fingerprinting subclonal tumor composition. Nucleic Acids Research, 41(17): e165-e165.

Supplementary Text and Input formats of all 12 methods are listed as separate PDF file.