

Resource Summary Report

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Minimal Event Distance Aneuploidy Lineage Tree (MEDALT) inference based on single cell copy number profile

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Proper Citation

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Protocol Information

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Authors: Fang Wang, Qihan Wang, Vakul Mohanty, Shaoheng Liang, Jinzhuang Dou, Jincheng Han, Darlan Conterno Minussi, Ruli Gao, Li Ding, Nicholas Navin, Ken Chen

Summary: This protocol describes two innovative algorithms: 1) A minimal event distance aneuploidy lineage tree (MEDALT) inference algorithm allows implementing genetically meaningful distances and is scalable to current single-cell datasets containing thousands of cells, and 2) A statistical routine, Lineage Speciation Analysis (LSA), enables prioritization of CNAs and genes that are non-randomly associated with the observed lineage expansion and thereby are potentially functionally important.

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