

SNV **Loss** **Gain** **CNLOH**

Diploid region

Variant

The diagram illustrates four types of copy number variations (CNVs) in a diploid region. Each variation is shown in a pair of cells, with an arrow indicating the transition from the initial state to the variant state.

- SNV (Single Nucleotide Variant):** The initial state shows two gray bars (diploid region). The variant state shows a red star (variant) on the first gray bar.
- Loss:** The initial state shows two gray bars. The variant state shows one gray bar missing, leaving only one gray bar.
- Gain:** The initial state shows two gray bars. The variant state shows three gray bars (one extra copy).
- CNLOH (Copy Number Loss of Heterozygosity):** The initial state shows two gray bars. The variant state shows one gray bar missing and a red star on the remaining gray bar.

The diagram illustrates the construction of a phylogenetic tree from targeted scDNA-seq data. The top part shows a timeline of cell populations S1, S2, and S3 over time, with mutations (SNVs, CNLOH, GAIN) occurring at time points T^0 , T^1 , T^2 , and T^3 . The bottom part shows the step-by-step construction of the tree, starting from a Root node and adding mutations to create intermediate nodes, which are then compared to the observed data in S1, S2, and S3.

Top Panel: Timeline and Mutations

- Time Axis:** A horizontal line representing time, with vertical lines indicating the sampling points for S1, S2, and S3.
- Cell Populations:**
 - S1:** A cluster of cells, some normal (blue stars) and some cancerous (red stars). Targeted scDNA-seq of autosomal regions A, B, and C is performed.
 - S2:** A cluster of cells, some normal (blue stars) and some cancerous (red stars).
 - S3:** A cluster of cells, some normal (blue stars) and some cancerous (red stars).
- Mutations and Events:**
 - T^0 :** Germline SNP (blue star).
 - T^1 :** SNV (red star).
 - T^2 :** GAIN B (black bar).
 - T^3 :** SNV (orange star), SNV (yellow star), CNLOH A (grey bar).

Bottom Panel: Tree Construction

- Root:** The starting point of the tree, containing the Germline SNP (blue star) and regions A, B, and C.
- Step 1:** A mutation (SNV, red star) is added to the Root, creating a new node.
- Step 2:** A mutation (GAIN B, black bar) is added to the previous node, creating a new node.
- Step 3:** Two branches are shown, each with a mutation (SNV, orange star and SNV, yellow star) and a CNLOH A (grey bar).

The tree construction process is guided by the principle: "Grow previous tree with new mutations". The final tree structure is compared to the observed data in S1, S2, and S3 to determine the most likely phylogenetic relationship.

Figure 1: Genomic copy number analysis of three samples (S1, S2, S3) using a multi-cell approach. The figure shows bar charts of copy number across autosomal regions (A, B, C) for three samples. Sample 1 (S1) shows a normal diploid state (2 copies) across all regions. Sample 2 (S2) shows a normal diploid state (2 copies) across all regions. Sample 3 (S3) shows a normal diploid state (2 copies) across all regions. A legend explains the bar colors: blue for total reads, red for alternative reads, and grey for region coverage. A dashed box highlights the region coverage for Sample 3, showing a peak in total reads and a corresponding peak in alternative reads.