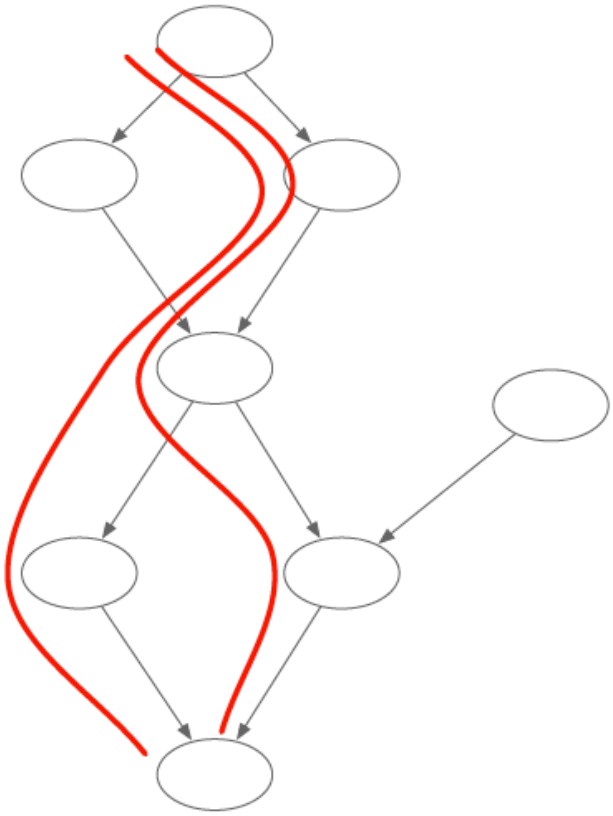

Merging of insufficiently different path sequences. Prior to path extension, all existing paths (shown as red lines) that presently terminate at the given node (bottom-most node) are compared in a pairwise fashion. A pair of paths are examined to determine if they are sufficiently different to remain as distinct paths, where sufficiently different is defined by the following parameters: '--max_diffs_same_path' (default: 2), '--min_per_id_same_path' (default: 95), '--max_internal_gap_same_path' (default: 10). Paths are defined as too similar if the following logical condition is met: there is no individual insertion or deletion that exceeds the --max_internal_gap_same_path setting, and either the percent identity of the alignment is at least the --min_per_id_same_path value or there are fewer nucleotide mismatches encountered than the --max_diffs_same_path value setting. If paths are deemed too similar, then the path with the greater read support is chosen and the lesser-supported path is discarded. If both paths have equivalent read support, then the shorter path is discarded. Using strict parameter assignments will result in a minimal non-redundant set of output assembled sequences, but a more permissive assignment is recommended in order to discover slight variants.