



Fig. 1. The original sequence has been artificially created by mimicking a likely real case as follows: in a starting sequence TTCAGTT the unit CAG has been expanded by a factor $(6 + 2/3)$, and then two point mutations have been added (an insertion and a substitution respectively in the third and fourth CAG). The autoalignment in phase 1 is illustrated by the various positions, along the sequence, of the scanning fork showing all the pairs of aligned indices $\alpha(k)$ and $\beta(k)$, with offset $\gamma(k) = \beta(k) - \alpha(k)$, for $k = 1, \dots, 17$. The chart collects for greater clarity all the pairs of aligned indices of the autoalignment. The hypothesized alignment in phase 2 (i.e. the SIP) between the model TR (obtained from the hypothesized expansion of a consensus) and a tract of the sequence, is illustrated by the links connecting the aligned bases. There is no link for the inserted base, and the dashed link indicates the point substitution.