1: Splitting of the sequence into windows

2: Clique partitioning of variables $C_i$

3: Construction of an LCM (DAG) for each clique of size $\geq 2$

4: Learning of parameters and imputation of values for each parent $P_j$

5: Validation of LCMs based on information criterion $C$ and update of the matrix of observations

6: Inside each window, construction of the FHLCM from the LCMs

7: Union of the FHLCMs over the windows