**Important notice regarding transmission tree and sequence simulation**

When building transmission tree from a transmission network, we assume that the nodes are transmission events and the leaves are sampling ~~removing~~ times (which may be diagnosis time of an individual, dying time or tend of simulation if the individual was still alive and not diagnosed).

When we have a dataset where a sampled individual can no more transmit (which may be interpreted as dying or the fact that someone who knows her/his status avoid to behave in a way s/he may transmit the infection), it is feasible to translate the transmission network in a binary transmission tree. However, when at least one individual transmit the infection after being sampled, the transmission tree is not feasible due to ngative branch lengths. Therefore, for an epidemic which takes into account such behaviour of transmission after sampling, it is advisable to simulate sequences at individual level specific because the use of a transmission tree to simulate the sequences is not