**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 and subsequently simulate molecular evolution across the transmission network. However, when at least one individual transmit the infection after being sampled, the transmission tree is not feasible due to negative values of 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 possible.

In Simpact to simulate trasmission tree, parameters need to be setup such that after all infected be diagnosed, and after diagnosed be on treatment and get viral suppressed to avoid next transmission after diagnosis events.

**Long branch lengths interpretations:**

Long branch in a time-stamped phylogenetic tree means that the two sequences (individuals) have common ancestor far in the past. Despite the Long Branch Length Effect well known, this can be interpreted as the existance of missing intermediate individuals who haven’t been sampled or the fact that an individual transmitted the infection after a period of time of being sampled.

**HIV phylodynamics modelling beyond the 90-90-90 target**

The establishment of the 90-90-90 target by UNAIDS (in 2013) was a big step towards the elimination of HIV infection in the World. It is an ambitious target by which in 2020 90% of PLHIV should know their HIV status, 90% of these who know their HIV status should be on treatment, and fromthese on treatment 90% of them should reach viral suppression.

However, in some countries (regions) it still not easy to get HIV test or to have easilly access to care and treatment after being diagnosed with HIV. This means that the target may not be achieved by all countries.

Knowing the HIV status can have an impact of transmission in a community, since someone who knows his (her) status can change his (her) behaviour to avoid getting the infection if s/he found her/him self HIV negative, or not to spread the infection of s/he found s/he is HIV positive. In addition, being on treatment after diagnosis is the best way combined with behariour change to ensure that the infection is not spreading.

Briefy, when we want to model HIV phylodynamics we intend to use the transmission tree (e.g.: papers of Giardina, Gabriel, ...), that approach assume that after being infected you’re removed, you cannot infect anymore [the goals of 90-90-90 target], which can be summarised as INFECTED-REMOVED. Thus, phylodynamics modelling with this approach can be seen as 90-90-90 because after being diagnosed by 90-90-90 target you cannot cause a new infection. However, a sampled individual can still infecting others due to several reasons, but on public helath point of view, not achiveing the 90-90-90 can be a cause of subsequent infections. In this situation where a sampled individual infect again, when we sample his/her recipients and construct a time-stamped phylogenetic tree, the branch lengths of recipients will be long if the ssequence of the donor is in the pool of sequence to analyse, or if s/he infect two/or more in different time intervals.

**AIM**: Show other potential explanations of long branch lengths and lessons we can get from them: when an individual has a short branch length but same internal node with an individual with long branch length this will may means that the individual with short branch length infected after being sampled.

Running Simpact to setup metrics of 90-90-90 target after 2020.

Revisit Birth-Death-SIR model in phylodynamics.