The history of genes

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The evolution of species can be traced back in history using the molecular changes in genes over time. This is modeled as a process of change along an evolutionary tree termed phylogeny. The two most important types of events are substitutions and indels (insertions and deletions) of nucleotides. Indel events are notoriously difficult to model and to reconstruct. Funded by SNSF grant 31003A_157064 (454'000 CHF between 2015–2018), Massimo Maiolo and Lorenzo Gatti – PhD students at the Applied Computational Genomics Team – have developed new methodology, which for the first time employs a mathematical indel model in order to find and align evolutionary related gene sequences and to infer their phylogenies (fig. 1). Building on this work, the research will continue to tackle a joint reconstruction of ancestral gene sequences and the phylogenetic relationships. New funding of 800'000 CHF was secured for 4 years (2018–2022) provided by SNSF grant 31003A_176316.