

The thesis deals with presence of runs of homozygosity, their origin and ways of their detection. Based on the analysis of two samples provided by the Institute of Neurology, University College London, we study differences in detection of runs of homozygosity between four different programs. The next part of the thesis is devoted to creating an original visualization for one of the used programs, namely BCFTools/RoH. This visualization is created in HTML and Javascript programming languages, thanks to which it can be opened in a web browser. The visualization enables display of the data in a non-traditional form and at the same time it preserves the biological context of the displayed data.