

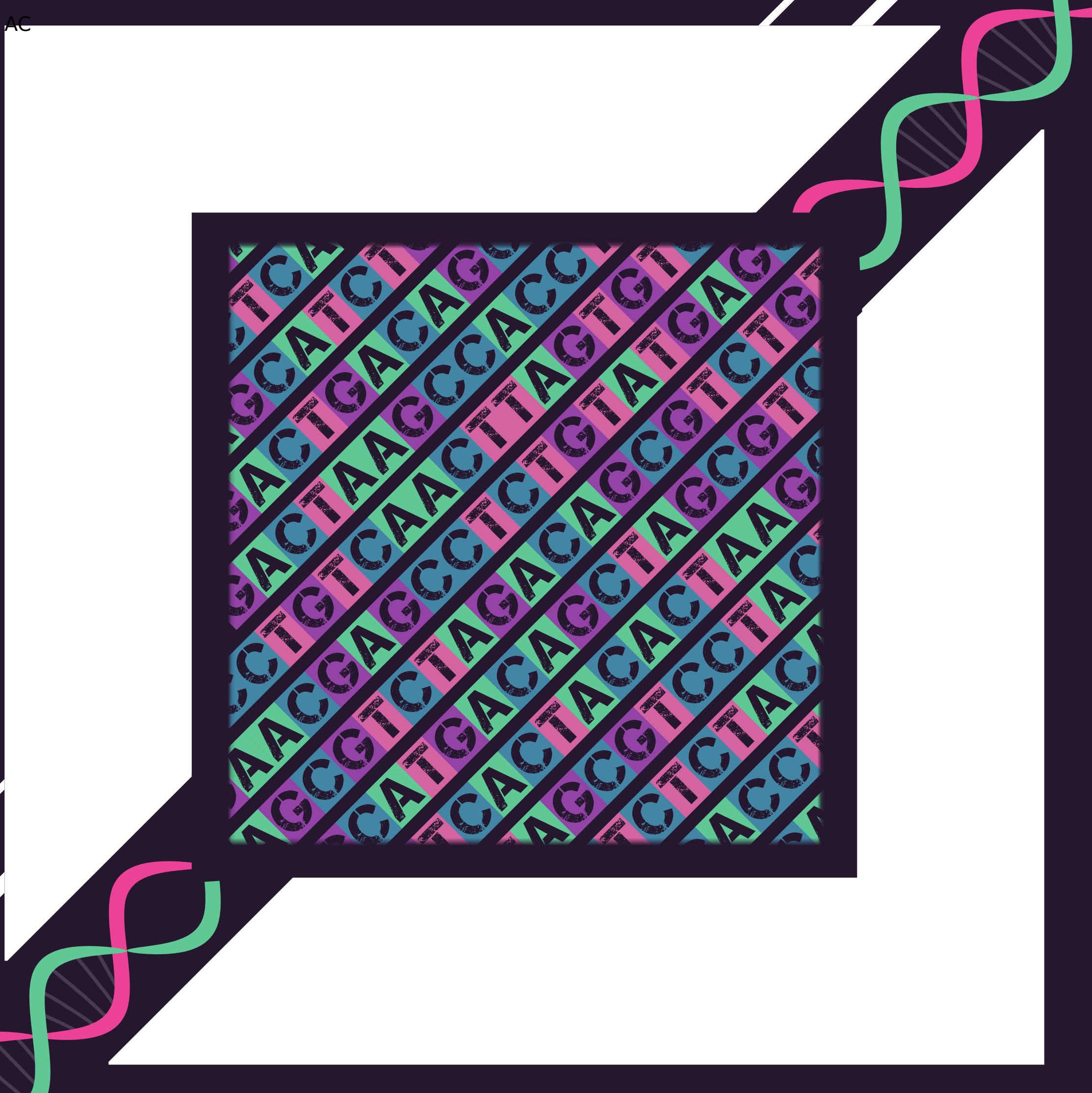
Genomic technologies are constantly evolving. Today, we produce a large amount of data and bioinformatics has become crucial for biology and medicine. Several free solutions already exist to process genomic data, but most of them are not-so-user-friendly command-line applications and require advanced computer skills. To help non-experts to analyze their data, several commercial companies are already on the move and are seducing people with nice graphical user interfaces. Labsquare would like to be an alternative: a non-profit organization which produces simple and accessible open source genomic GUI software for everyone.

Technology

We favour Qt framework - a GPL C++ framework which allows us to develop modern cross-platform applications. It is an alternative to Java for building modern user interface with advantage and power of C++.

Community

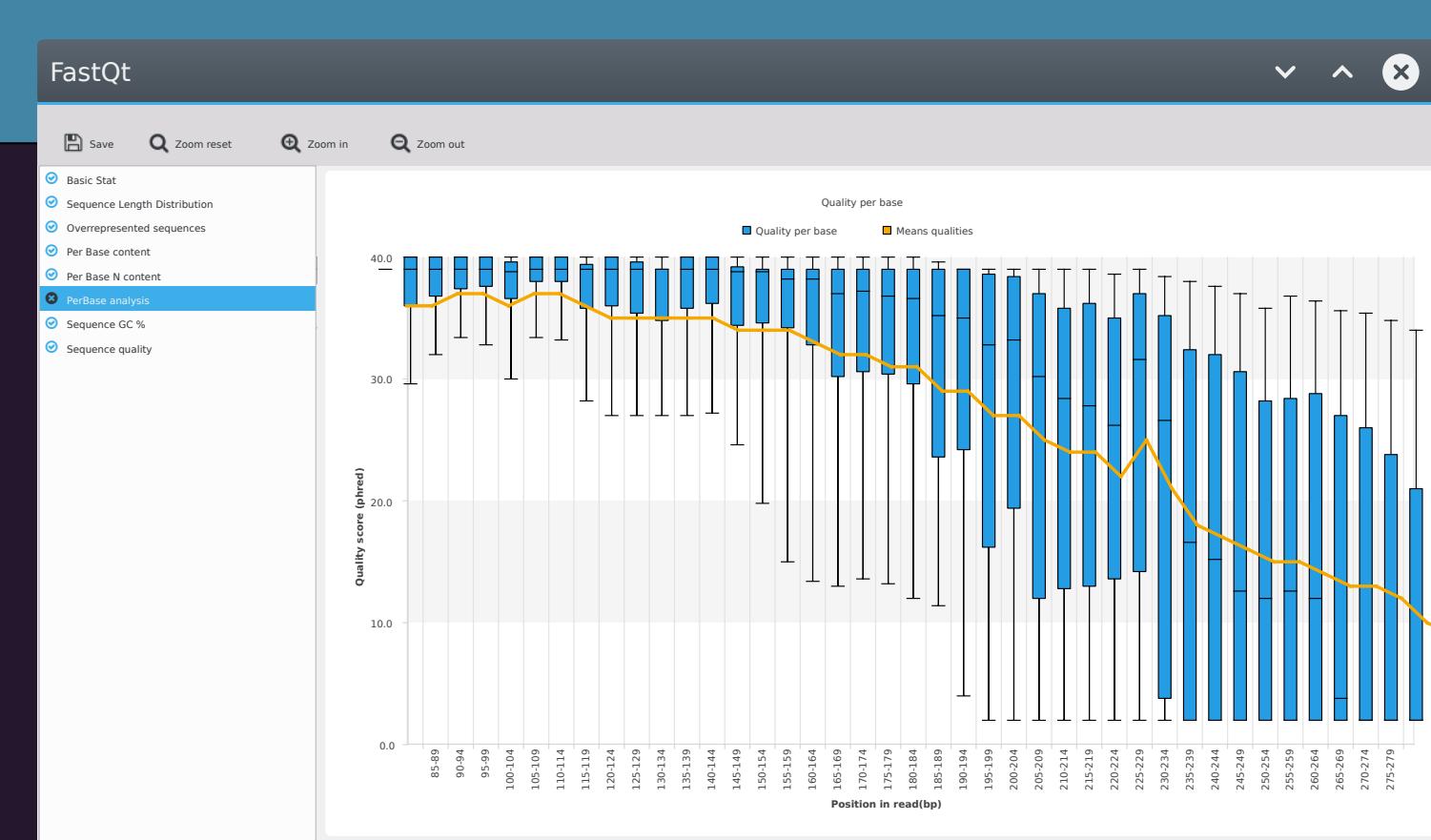
So far we are just a small team, but all skills are present. We are bioinformaticians, geneticists, physicians, developers, and designers. Our open source projects are available on GitHub and we are talking on #Gitter.



Labsquare
is a community of dedicated individuals focusing on development of simple and usable genomic software

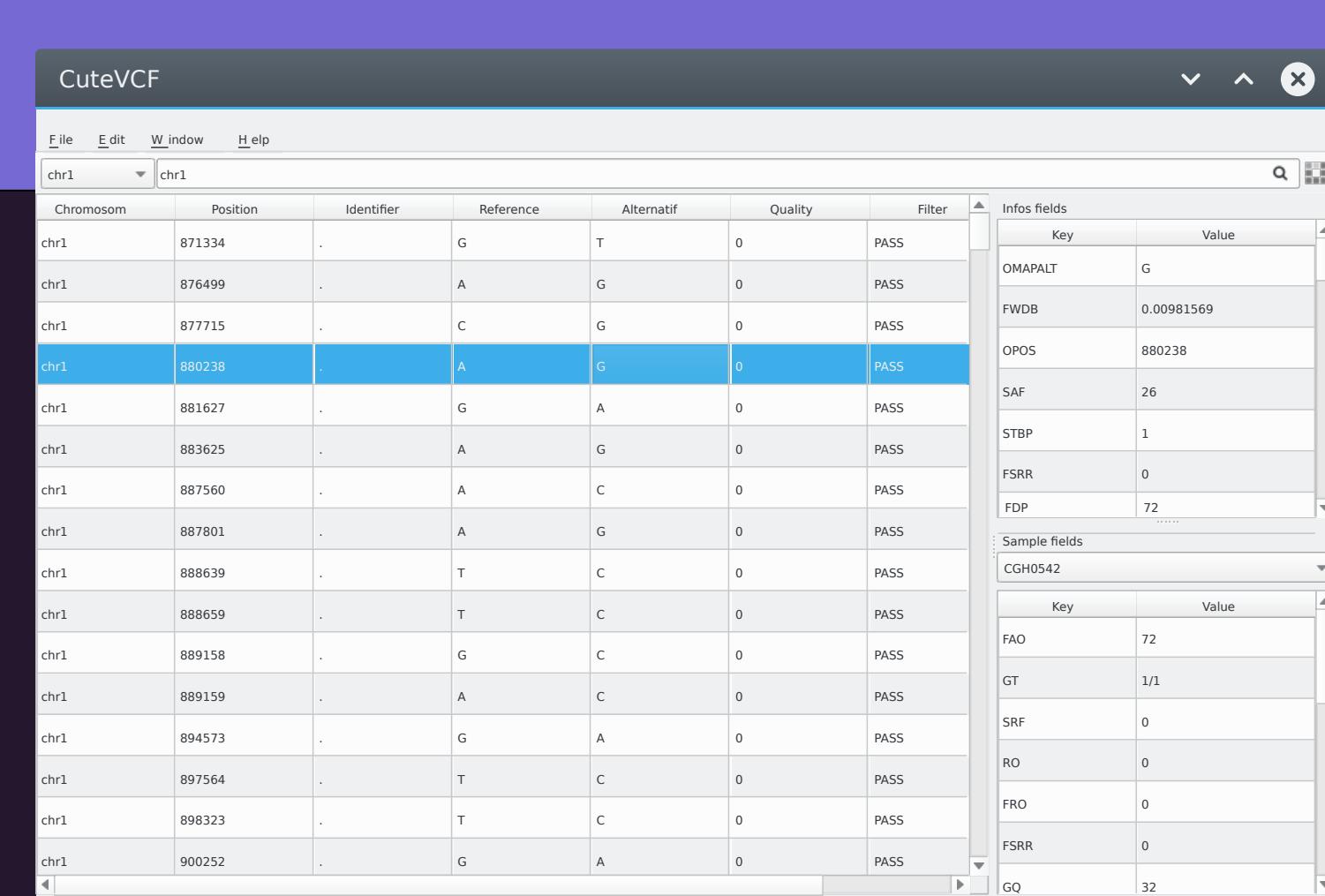
FastQt

FastQt is a fast, clean and intuitive tool designed to process FASTQ files. We developed it from ground up and it's taking a lot of inspiration by the famous FastQC app.



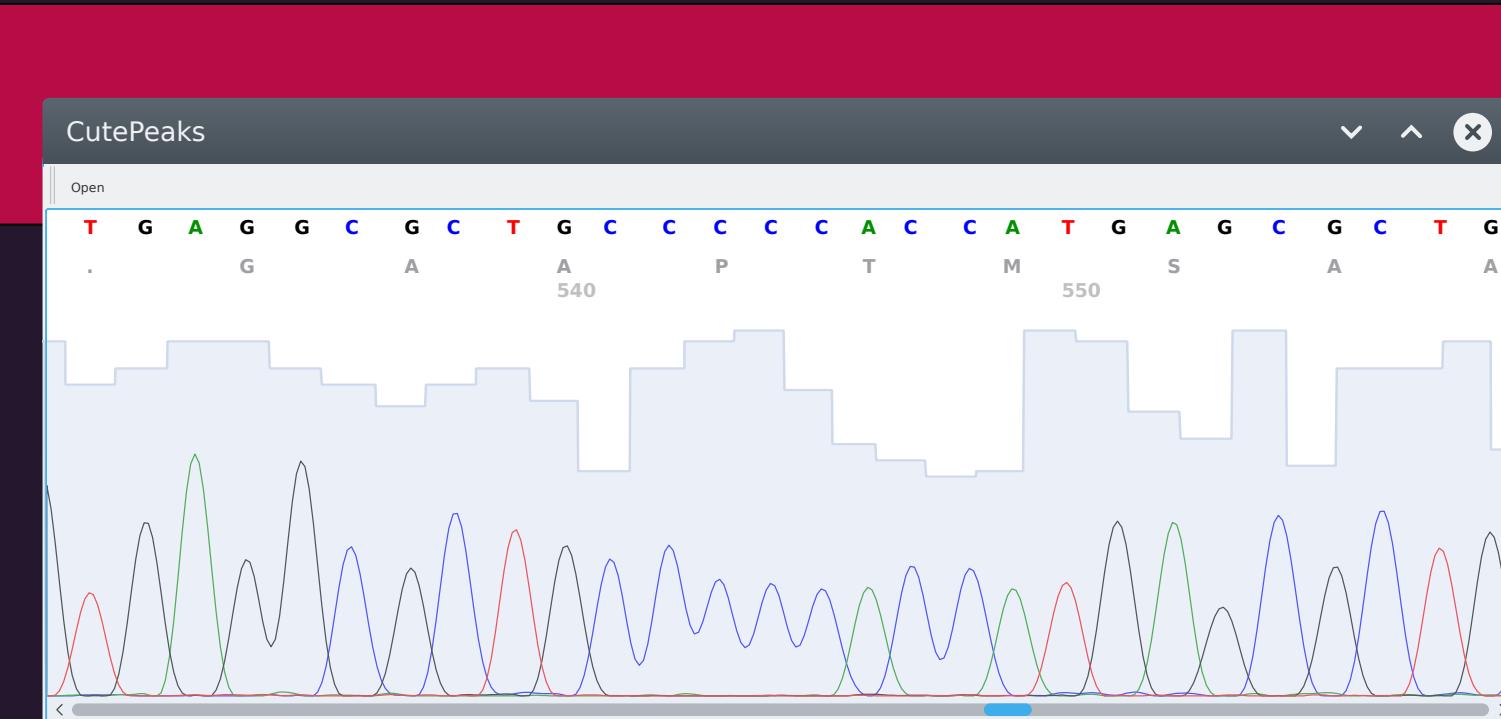
cuteVCF

cuteVCF is a simple and intuitive VCF viewer. We are also working on another similar app, inspired by Variant Tools.



cutePeaks

cutePeaks allows to display Sanger trace data in a fashion way. It supports AB1 and SCF trace file.



And other apps are under development... (a genome browser, a fasta editor, a pipeline launcher ...)