SYSTEMS AND METHODS FOR PROCESSING NUCLEIC ACID CHROMATOGRAMS

ABSTRACT

Computer systems, computer program products and methods for processing an input nucleic acid chromatogram having a plurality of substantially simultaneous traces. Each trace in the plurality of traces has a plurality of datapoints. Each respective datapoint in each of the plurality of datapoints represents a signal amplitude at a position in the trace corresponding to the respective datapoint. A first peak is identified in a first trace that is substantially overlapping a second peak in a second trace in the plurality of traces. The first peak is outputted to a first output homozygous representation and the second peak is outputted to a second output homozygous representation. The first output homozygous representation is a first homozygous sequence representation or a first homozygous nucleic acid chromatogram corresponding to the input nucleic acid chromatogram. The second output homozygous representation is a second homozygous sequence representation or second homozygous nucleic acid chromatogram of the input nucleic acid chromatogram.

Fig.1