Title: Combination of expert decision systems with artificial intelligence leads to superior accuracy of automated prediction of clinical effect of copy number variation

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Interpretation of clinical impact of large mutations is a difficult task mainly due to the size of affected genomic content. In the past years, several tools have been built for interpretation of single nucleotide polymorphisms (SNP), however not so many for copy number variants (CNV). In this work we present two methods for pathogenicity prediction of CNVs: an ACMG based method which follows strict set of rules aggreed upon by a large consortium of scientists and a machine-learning based method ISV (Interpretation of Structural Variation). We show that a joint use of both tools yields superior performance compared to using the tools alone. We believe that using predictors utilizing different data sources should create a more robust overal predictor, which can be used in practice by laboratory scientists to help with the laborious interpretation process.