Screening for somatic mutations in cancer has become integral to diagnostic and target evaluation for personalized therapeutic approaches. *arrayMap* is a curated oncogenomic resource, focusing on copy number aberration (CNA) profiles derived from genomic arrays. Whereas this database is based on reprocessed probe data sets, the parental project, *Progenetix*, allows for genome variant analysis from additional sources and serves as metadata reference. Both resources apply automated and manual data curation methods for content generation.

For interoperability of clinical data curated from e.g. NCBI's Gene Expression Omnibus (GEO), EBI's ArrayExpress and targeted publications, substantial efforts have been done in data standardization. Particularly, the resulting comprehensive resource consisting of *Progenetix* and *arrayMap* contains information for more than 400 ICD-O entities and 63'000 genomic array profiles. Existing standards such as ICD-O have proven to give a good description of a cancer entity based on the morphology and topography of the sample. Nevertheless, it is not a builded hierarchical classification and some information is not captured.

Since ontology based codes are necessary to cross resources the use of NCIt is optimal, providing hierarchical reference terminology. Hence, for better data exploration original resources need to be remapped through services such as *OxO*. Still further curation is needed indicating the urge need to refine services and propose new solutions to improve data integration in biomedical settings.