

An illustration of the strengths of RDF-based multilayer network-analysis is the work I have done in the Sanger Institute*. When analysing predicted altered and/or de novo transcription factor binding sites (TFBS) by single-nucleotide polymorphisms (SNPs) in non-coding regions of over 1300 melanoma-patients, no overrepresented TFBS were found. However, when linked to a triple-store of TF-families and a triple-store of TcoF –containing TF-interacting proteins and co-factors- we found that there was a clear overrepresentation of TFs, binding to the transcription co-activator NCOA6. Further analyses showed more evidence of the importance of this protein in familial melanoma (e.g. co-segregation in melanoma-prone families). Without the multilayer network-analysis, such results are often not found and without RDF, different databases and -sources would be much harder to integrate for (exploratory) analyses.

*unpublished data, discretion appreciated