

# Integrating Nencki Genomics webservice via Taverna workbench

Izabella Krystkowiak, Michal Dabrowski\*  
Nencki Institute of Experimental Biology, Warsaw, Poland.  
*\*presenting author, e-mail: m.dabrowski@nencki.gov.pl*

Under the Nencki Genomics project (<http://www.nencki-genomics.org>), we developed a set of webservices for analysis of gene co-expression, cis-regulatory regions, and functional annotations; on the basis of user-supplied genomic or expression data and the large body of public regulatory genomic data provided by the Nencki Genomics Database [1]. The webservices use the well-defined SOAP/WSDL interface and are divided into two sets: genomic and expression. The genomic webservices provide functionalities of mapping regulatory areas to genes, intersecting regulatory areas, and intersecting areas with known TFBS motifs (both Jaspar and Transfac), identified genome-wide. Notably, we provide a webservice function, which plots a graphical representation of selected NGD content in the flank of transcription start site of a chosen gene. The expression webservices can be chained to provide a typical workflow of analysis of transcriptomic data, from pre-processed gene expression data (probes/genes x conditions), through probesets mapping and data transformation, to identification of differentially expressed genes, clustering and visualization. At each step of the analysis, the results can be returned to the user as a TSV file, piped to the next step, or stored in the underlying databases (providing access right control) for future use, sharing the data with others, or making them public.

Taverna Workbench (<http://www.taverna.org.uk/>) is a rapidly developing open-source workflow management system, which we use for the integration of the Nencki Genomics webservices. Taverna's graphical user interface (GUI) makes these functionalities accessible to a broad biological community of users.

[1] Krystkowiak et al. Nencki Genomics Database – Ensembl funcgen enhanced with genome-wide TFBS motifs, intersections and user data. *Database*, under revision.