**IDseeqer – Connecting shared data in 2 clicks**

***Problem statement:*** Databases of experimental and computed data are a growing resource for shared experimental data. Deposited datasets are usually linked to the specific or a global standard current at the time of deposit. These standard IDs are rapidly changing with updating genome annotations disguising the existing link between the sequences behind IDs. The manual connection of distinct ID systems as well as obsolete IDs is a highly time consuming and difficult task that leads to incomplete and abandoned analyses.

***API Scope:*** In order to automatically connect datasets based on sequence ID systems, we are developing the program IDseeqer that will retrieve a genetic/proteomic sequence from a list of mixed IDs and compare them to the current standard. The user will be able to install packages and templates for collecting the sequence for all datasets that need to be connected (click1) and align them to IDs of the current ensembl genome standard (click2). The result will be the linkage of multiple datasets to the same ID system and therefore the convergence of attached data.

***Significance:*** IDseeqer is a tool that enables the connection of experimental data to functional annotations of multiple databases and other experimental data in with little effort. This is an immense saving of resources and time and will increase the speed of knowledge discovery in new datasets as well as increase the reuse of existing data sets irrespective of the data set size.