PlutoF – cloud database and computing services for the biologist

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PlutoF (http://plutof.ut.ee) is a platform providing cloud database and computing services for taxonomical, ecological, phylogenetical, etc. research. It allows to address integrated questions in ecology and coevolution of taxa as well as manage different types of species occurrences, viz. preserved specimens, DNA sequences, human observations, etc. PlutoF cloud comprises of a complex relational database model and a web-based workbench built upon it as a thin client. It also includes several public web sites for displaying and searching the data. For example the Estonian eBiodiversity database (http://elurikkus.ut.ee) gathers all available biodiversity data (collection specimens, observations, references, molecular data, multimedia, Red List status, etc.) linked to taxa present in Estonia; UNITE database (http://unite.ut.ee) provides reference DNA sequence dataset and software tools for molecular identification of fungi.

PlutoF workbench features a login system and workgroup management allowing its users to:
• manage ecological studies using the hierarchical study/plot/sample model;
• add and edit various taxon occurrences;
• manage classification, names of the taxa and scientific collections;
• use the analysis module to examine molecular sequence data and their associated metadata. Software currently available includes massBLASTer, Fungal ITS Extractor, Chimera Checker and 454 pipeline for pyrosequencing data;
• upload molecular sequence data into UNITE database and annotate fungal DNA sequences of International Nucleotide Sequence Databases (INSD) for quality and additional metadata.

PlutoF web interface uses the following web technologies: PHP (PHP: Hypertext Preprocessor), HTML (HyperText Markup Language), CSS (Cascading Style Sheets), AJAX (Asynchronous JavaScript and XML), JavaScript and SQL (Structured Query Language). Database management system involves MySQL 5.0.77. Software packages of the analyses module are mostly written in Perl.