

observation materials available in the reserve, to facilitate access to them, to preserve these observations from loss, and to perform an inter-related analysis of long-term series of observations. At the moment inventory lists of higher vascular plants and herbarium of the Barguzinsky Reserve are being prepared for publication in GBIF.

## **Data lineage for Baikal microbiome study**

Fyodor Malkov, Alexey Shigarov, Evgeny Cherkashin

Irkutsk Scientific Center, Irkutsk, Russia  
iksut@ya.ru

## **Отслеживание происхождения данных в исследовании микробиома Байкала**

Ф.С. Малков, А.О. Шигаров, Е.А. Черкашин

ИНЦ СО РАН, Иркутск, Россия  
iksut@ya.ru

The Baikal microbiome study is being conducted in Limnological Institute of SB RAS, the study is based on the next-generation sequencing data analysis. As a result, the study generates a big volume of metagenomic data. The work considers issues of the data lineage for Baikal microbiome study with the next-generation sequencing, from a moment when researchers describe a sample of water or bottom sediments to publication of research results. We propose a service for data lineage based on storage and execution of metagenomic processing and analysis pipelines. The service provides reliability and reproducibility of published research data.

## **Development of regional biodiversity portal in Khanty-Mansi Autonomous Okrug-Yugra**

Nina Filippova, Ilya Filippov

Yugra State University, Khanty-Mansiysk, Russia  
filippova.courlee.nina@gmail.com

# Разработка информационного портала “Биоразнообразии Югры”

Н.В. Филиппова, И.В. Филиппов

Югорский государственный университет, Ханты-Мансийск, Россия  
filippova.courlee.nina@gmail.com

Khanty-Mansi Autonomous Okrug – Yugra located in the central part of Western Siberia. Biodiversity-related studies are relatively young there in line with intensive industrial development of the region in recent decades. The region poses a few of biological collections within the Universities and Nature Reserves. Still, the Department of Natural Resources of Yugra pays considerable attention to the sustainable use of natural resources. The advance of computer and Internet technologies produces response in biodiversity science, thus biodiversity informatics discipline developing quickly over last decades with considerable results in development of protocols, standards and global platforms for integration of biodiversity data. The data flow from local, regional and national nodes to global platforms (like GBIF) where integrated data are broadly available. On the local scale, the employment of biodiversity informatics methods for storage, analyses and publication of biodiversity data greatly improves the quality of work. Organization of biodiversity portals promotes education and opens the realm of science to citizens. Due to these reasons organization and development of biodiversity portal in Yugra region would be an important and timely task. Previous experience of biodiversity information systems in Yugra was only initial. The program on digitization of observations of Red Listed species was launched in 2010 under support of the Department of Natural Resources. The information system UGRABIO developed through this project currently includes about 3 thousand observations. Another case of digitization was shown by a biological collection of Yugra State University with its database based on Specify product and available online through its web version. Some collections of Nature Reserves have their catalogues in digital form. The demand of collections digitization seems well understood as shown at regular workshops on Biological collections management held in Khanty-Mansiysk. Recently biologists curating several biological collections in the region started a project on a regional biodiversity portal (YugraBio). The already developed product Symbiota – a package of web tools for integration of separate collections databases will be used for the portal development. The YugraBio project will include several stages: 1)

a metadata database of biological collections in Yugra will be developed, 2) major biological collections will be digitized, 3) algorithms and guidelines will be developed during the digitization, 4) the overall structure of the portal will be developed, 5) the portal will be linked to the national IPT node for export to national and international (GBIF) portals, 6) finally the workshops and seminars for information dissemination should be organized. The collected massive of data in the portal would give new opportunities for biodiversity research and sustainable management of nature resources in the Yugra region.

## Development perspectives of CRIS

Denis Davydov<sup>1</sup>, Eugene Borovithcev<sup>2</sup>, Roman Fedorov<sup>3</sup>, Nadezhda Konstantinova<sup>1</sup>, Alexey Melekhin<sup>1</sup>, Sergey Schalygin<sup>4</sup>

<sup>1</sup> PABGI KSC RAS, Apatity, Russia  
d.disa@mail.ru

<sup>2</sup> INEP KSC RAS, Apatity, Russia  
borovichyok@mail.ru

<sup>3</sup> Matrosov Institute for System Dynamics and Control Theory SB RAS, Irkutsk, Russia  
fedorov@icc.ru

<sup>4</sup> TAMUCC, Corpus Christi, USA  
got.lifemusic@gmail.com

Cryptogamic Russian Information System - CRIS (<http://kpabg.ru/cris>) is devoted to cataloging biodiversity information of the cryptogamic organisms such as algae, fungi, lichens, and bryophytes. In contrast to Darwin-Core principles with its single species record as a baseline, CRIS is working with multispecies records. CRIS allows for users to enter different types of data such as labels of herbarium specimens, literature references, media files etc. Rapid increase of records number, diversification of types of materials, complication of the structure of the record forced us to switch from CMS Drupal to modern Node.js. The major problem in CRIS is to fix issue related to slow geo-searches, which are overloading server at the moment. Mass processing of data and other features will be convenient improvements of the system. The modified version will have intergroup search; this will be accomplished by making connection between different sections of CRIS. In contrast to the old version of the CRIS based on Drupal, new version will have universal numbering system with “Universal herbarium specimen” (UHS) as a core. UHS from one herbarium may be easily converted into record of another herbarium, when for example