BioVeL workshop at the ForBio annual meeting, Oslo, 5 March 2013

Mattias Obst (<u>matthias.obst@bioenv.gu.se</u>)
Department of Biological and Environmental Sciences, University of Gothenburg

Title: Workflows for data refinement and ecological niche modelling.

Registration: register at https://nettskjema.uio.no/answer/53406.html to secure a seat. Please note that the number of participants is limited to 15.

Time: March 5, 15.30 – 18.30 at Quality Hotel 33, Oslo. Please note that the workshop is part of the ForBio annual meeting (www.forbio.uio.no/events/meeting/2013/index.html).

Requirements: Bring your own laptop. All workflows offered will be browser- based and don't need any desktop installations. A sample data set will be provided with each workflow.

Background: In the last two decades the relationship between biodiversity and ecosystem function has become a central issue in ecology, while biodiversity loss has been identified as a major driver of ecosystem change. As a result, ecological research transforms into a species-rich scientific discipline with increased focus on the ability to document, study, and predict the biodiversity composition in ecosystems. However, the analysis of patterns of biodiversity over large temporal and spatial scales is still very difficult to achieve as it requires biologists and environmental scientists to integrate their expertise, data, and methodologies across the traditional biological disciplines. The Biodiversity Virtual e-Laboratory, BioVeL, addresses this challenge (for details, see www.biovel.eu). In the BioVeL, scientists and computer engineers are working together to develop tools for pipelining data and analysis into efficient analytical pipelines, called workflows. Workflows are complex digital data manipulations and modelling tasks that execute sequences of web services. BioVeL designs and deploys such workflows for a selected number of important areas in systematic, ecological, and conservation research, e.g. for the analysis of data sets with ecological, taxonomic, phylogenetic, and environmental information. The workflows allow the researcher to (i) explore, access, refine, and format large data sets from major data providers, (ii) combine disparate data sets with the researchers' individual data, and (iii) run complex and computationally intense analytical cycles. The workshop is a collaboration between SwedishLifeWatch (http://www.slu.se/lifewatch), NordicLifeWatch (http://www.lifewatch.eu/en GB/joint-nordic), and BioVeL (www.biovel.eu).

Program

In session 1 we will give an overview over SwedishLifeWatch (http://www.slu.se/lifewatch), NordicLifeWatch, and BioVeL, and demonstrate newly released workflows for taxonomic data refinement, ecological niche modeling (and possibly phylogenetic inference), together with the presentation of scientific showcases based on these workflows.

In session 2 we will offer a hands on training where participants will learn to use these workflows and run scientific analysis on their own laptops.

In session 3 we will discuss possibilities for individual research projects by the students and how they can be supported.