



Project no. 018340

Project acronym: EDIT

Project title: Toward the European Distributed Institute of Taxonomy

Instrument: Network of Excellence

Thematic Priority: Sub-Priority 1.1.6.3: "Global Change and Ecosystems"

C5.072 Dynamically link GBIF data to core geoplatform allowing GBIF data to be visualised in addition to custom user data

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Duration: 5 years

Organisation name of lead contractor for this component:

14 RMCA

Revision final

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Dissemination Level		
PU	Public	X
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

Introduction

The EDIT core geoplatform services (such as the mapViewer tool) are useful largely because they are able to communicate with other services and tools on the Web. For this reason, the EDIT software component development is always modular (for easy adding of new components) and standards-compliant (for example adhering to the WMS/WFS standard for geographical data interchange).

One of the richest sources of biodiversity and taxonomic data on the Web is the GBIF portal, tapping into a wealth of specimen and species occurrence observation records from institutions all over the world. It was clear from the beginning of the EDIT geoplatform work that this resource could greatly enhance the usefulness of the taxonomic tools. User data points could be visualised along with the GBIF records for the same taxon to assess if the new fieldwork yields any new insights in the geographical dispersion.

Connecting to GBIF

So from the early on GBIF integration was envisaged, though the exact connection path has changed during (and due to) the technical development.

At first the Generic Query Tool (GQT for short), developed within SYNTHESYS NA-D, was scheduled to provide the link. This Tool can connect in a transparent manner to all sorts of biological data provider services, through different standard protocols (DiGIR, TAPIR and BioCase). See : <http://synthesys.africamuseum.be/GQT.html>

Tests were conducted and showed some promise - a tribute to the standard-adherence of the software development within both SYNTHESYS and EDIT. The GQT could interact with the mapViewer for displaying the results, through the WMS/WFS (and other) protocols.

However further development on the EDIT mapViewer tool saw the ending of Mapbuilder development and support. Until then, Mapbuilder (an AJAX library for building Web Mapping clients inside a browser) was the prime open-source framework for the mapViewer development. The decision was taken to move the mapViewer tool to the Openlayers framework, to ensure continuity in support and feature development (see : <http://openlayers.org/>).

In the OpenLayers framework, a direct link to GBIF was easier to configure than any other connection. So the mapViewer tool now uses the GBIF tools API to present the user with a connection to this data source (Fig. 1).

Now, the GBIF data for the same species (or higher taxon) can be added to the user's data points and visualised in the mapViewer. The symbols for the GBIF data points stems from the GBIF API, the user data points symbolisation can be adapted to match (or contrast) the GBIF points (see Fig. 2).

At lower zoom levels, the GBIF data points are aggregated into blocks for clarity. The user data point remain visible (not aggregated) for comparison (Fig. 3)

Thus, the full wealth of GBIF information is brought to the mapViewer tool in an easy to use and responsive way.

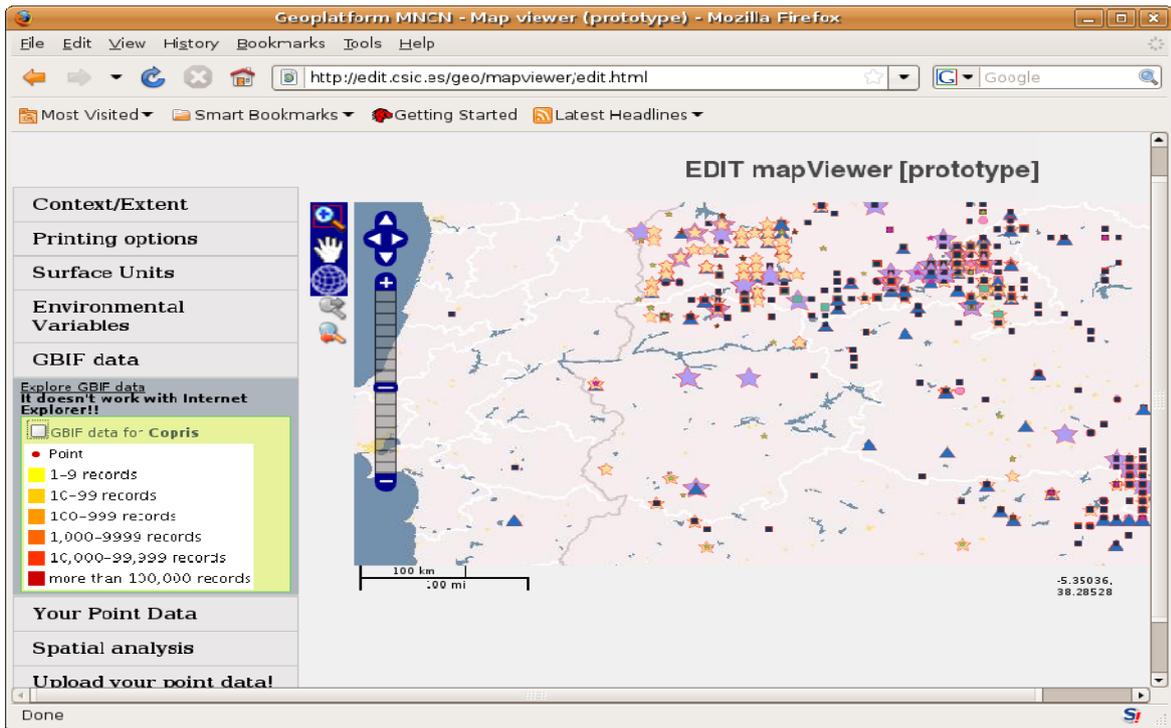


Fig. 1: The user's data points uploaded into the mapViewer, without the GBIF data. At the left the link to GBIF is visible. The symbols for the GBIF data points and the aggregation colouring scheme stems from the GBIF API.

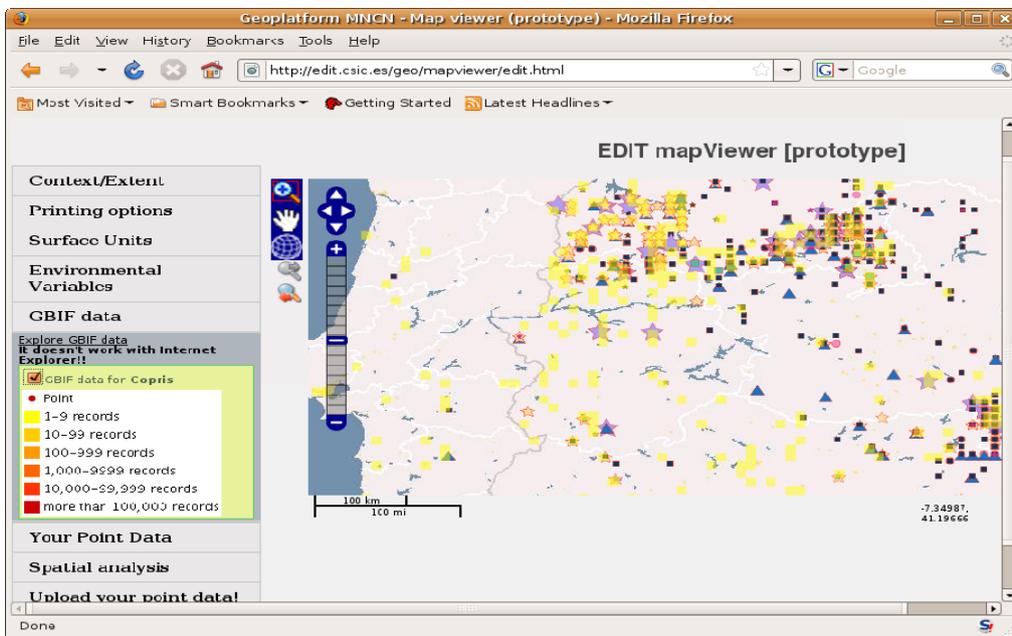


Fig. 2: Addition of GBIF data aggregations (yellow & orange squares), allowing comparison between new (user) and existing (GBIF) data records.

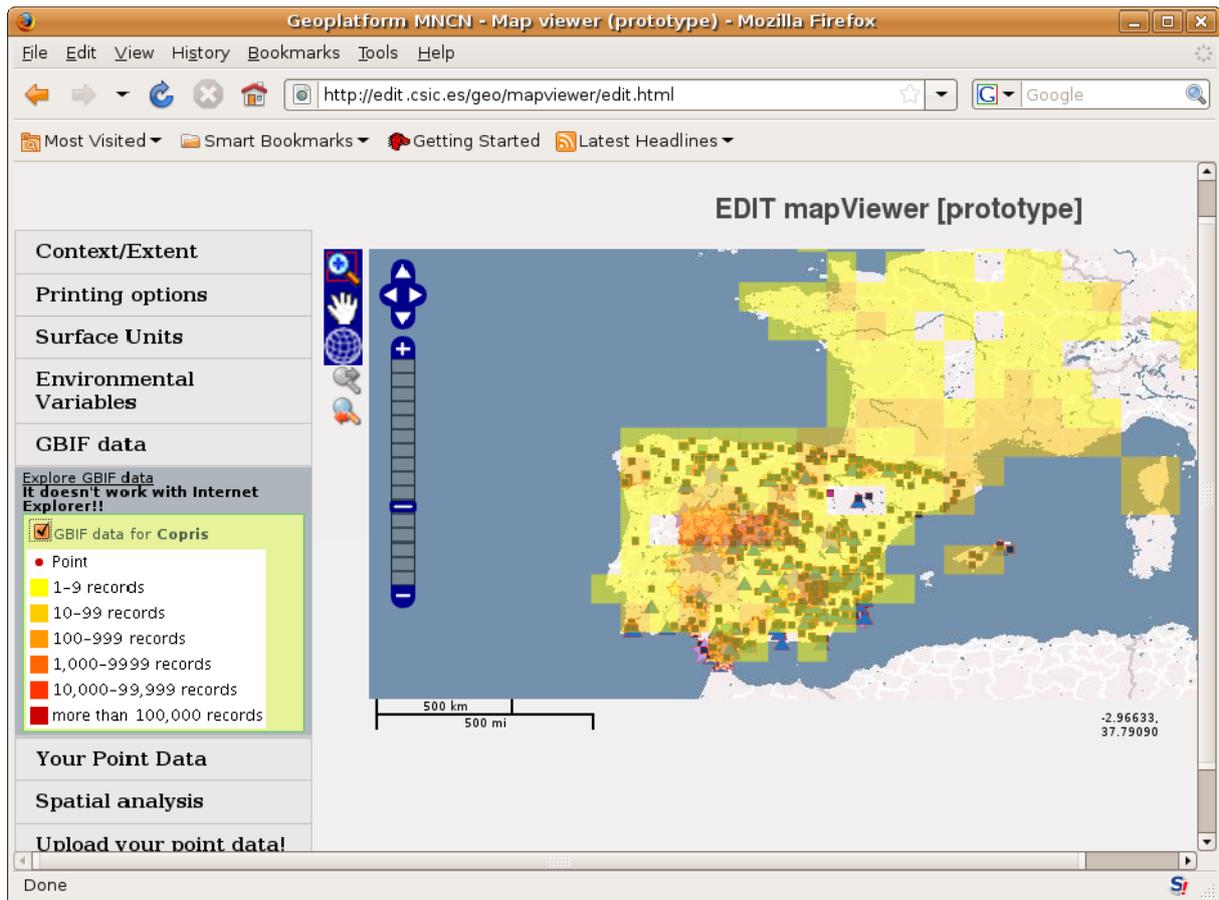


Fig. 3: At lower zoom levels, the GBIF data points are aggregated into blocks for clarity. The user data point remain visible for comparison.