D2.1 Use Case Requirements Specifications

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Deliverable Documentation

The Use Case Requirements Specification (**EuBrazilOpenBio deliverable D2.1**) covers the identification, analysis and discussion of use cases and requirements that will drive the implementation, integration and deployment of the EuBrazilOpenBio platform. This deliverable is expected to be a *living document* and it has been implemented in a form of a wiki which is updated and improved continuously. This implies that: *(i)* this document is only intended to provide its readers with a brief description of the Wiki, and *(ii)* the actual deliverable is available at:

http://wiki.eubrazilopenbio.eu/index.php/Use_Case_Requirements_Specification

This Wiki page is organised in a number of main sections:

- Section 'Description of the Use Cases' presents the use cases that will be addressed in the project, including a detailed description of the requirements for implementing the use cases from the point of view of performance, security and usability. This section also describes many technical details that will lead the implementation of the use cases, such as the relation to standards, the metrics that will be used to evaluate the realization of the requirements, and the moment in the lifecycle of the project when the e-infrastructure will be ready to support the requirement.

- Section 'Resources Inventory' introduces the different resources (e.g. data sources, applications) that will be available to the EUBrazilOpenBio users, as well as the tools that will support the deployment and operation of these resources in the e-infrastructure. Basically, the section consist describes the different types of resources needed to implement use cases and points out to the sections in the wiki where the resource inventory is detailed.

- Section 'Procedure for the identification of requirements' describes the procedure that has been used to gather the requirements, the different sections of the requirement specification, and the key persons and tools that support this activity in the project. Requirements are analysed using a standardised form that includes description, relations to standards, references, implementation information (to further explain or guide the platform developers), quality metrics (to measure the degree of fulfilment) and required date

- Section 'Requierements' that describe the 13 requirements identified by the use cases (4 for the Catalogue of Life and 9 for the Ecological Niche Modelling). Those requirements are basically high-level functionalities required to implement data browsing, data quality improvement and data processing required by the use cases. Notwithstanding the requirements are described through examples from the use cases for better understanding among the consortium, they are considered in a broad way to fulfill more general use cases.

The initial list of requirements (i.e. requirements identified at December 2011) focus on needs such as:

- The access of fundamental biodiversity data, such as the Catalogue of Life, GBIF, Brazilian Flora Checklist or SpeciesLink, from within the applications in the platform.

- The execution of pipelines of computationally-intensive searching and cross referencing actions, for the different taxonomical databases and with the objective of identifying missing entries and incoherences.
- To ensure a reasonable Quality of Service by providing scalability on the resources to access or process the data available in a timely manner.
- To provide a framework for the generation of models through different algorithms and by allowing those models to be tested and projected into different environmental scenarios.
- To provide the means to store and share models with different users and in different sessions, avoiding the recalculation of them.
- To provide the means for uploading own data to be used in the modelling of the species occurrence maps.
- To link with the processing services of the different tools and data sources identified.

Through the implementation of those requirements EUBrazilOpenBio will provide a platform that could be used to integrate taxonomical data, link to occurrence maps, compute probability models and project them on new scenarios.