

# A resource ontology for bioinformatics Resourceomes

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## Motivation

Bioinformatics constitutes a very dynamic and multidisciplinary galaxy in the scientific universe. At the dawn of the "omics" age it was defined as a discipline intended to manage and analyze the exponentially growing amount of biological data. Nowadays it has become hard to image genomics, systems biology, and other emerging fields of the modern biology, disjointed from bioinformatics. Bioinformatics itself represents one of the forces driving the paradigm shift of science toward e-Science. Beside "data deluge" and "information overflow", it's straightforward to figure out a similar condition also for knowledge. Actually we are witnessing a fast increasing production of scientific literature and the blooming of knowledge representation efforts (i.e. biomedical ontologies). Therefore, we could metaphorically depict bioinformaticians drowning in the ocean of resources (e.g. databases, articles, programs) developed from themselves. In general, the quest for the "right" resource has become a very demanding and time-consuming task. It's almost impossible for a human scientist to follow the evolution of the general field. The tracking of new resources, appeared in a limited research sector, represents already a challenging issue. In [1] we defined "resourceome" the full set of bioinformatics resources and invited the community to organize a general, machine-understandable, index of bioinformatics resources. Such an index should also take into account the semantic relationships between resources.

## Methods

Here we adopt the same term but with the uppercase R Resourceome, to identify the ontological representation of a typically huge set of resources. Aiming at the fulfillment of a general index of bioinformatics resources, we can foresee its bottom-up formation process. Individuals and special interest groups build their limited and probably overlapping Resourceomes, which subsequently could be shared, merged and integrated into a general one. In a Resourceome the knowledge of a domain is organized into an ontology, and the resources related to a concept of the domain are directly connected to that concept. "In-vivo" and "in-silico" scientists can easily navigate and "reason" through the semantic networks connecting resources and domain's concept. A single scientist could adopt a Resourceome to intuitively organize his/her perceived knowledge of a domain and the related preferred resources. We can naturally image Resourceomes also at the heart of next generation bioinformatics cyberinfrastructures. The adoption of semantic web technologies permit to arrange the concepts of the domain and resource's metadata, together with their relationships. Software agents, beside supporting the building and management of the ontology, permit to keep it "alive" and will support users in the navigation and queries.

## Results

We can reasonably assume that most of the peer-reviewed articles published in bioinformatics journals are intended to present new databases, algorithms, programs and other computational resources. Therefore, to provide also numerically the perception of the growth of the bioinformatics resourceome in the last years, we performed an analysis on the number of new bioinformatics journal and on the amount of published pages and articles for the most significant ones. Then, we developed a resource ontology to classify bioinformatics resources and to exploit their typical semantic relationships. Such a general classification, orthogonal to the domain ontology, is intended to be adopted in Resourceomes to describe, also visually, the type of the resources connected to concepts of the domain.

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**References**

1. N. Cannata, E. Merelli, and R. B. Altman. Time to organize the bioinformatics resourceome. PLoS Comput Biol., 1(7):e76, 2005.

**Supplementary informations**

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