



# BIOINFORMATICS DATA ANALYSIS WITH SEMANTIC WEB TOOLS: GENERAL PRINCIPLES AND APPLICATION TO THE REDUCTION OF METABOLIC NETWORK CANDIDATES

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le 10 mars 2015 16h00

ENS Rennes, Salle du conseil  
[Plan d'accès](#)

**Intervention d'Olivier Dameron (Université Rennes 1 / IRISA)**  
**Séminaire du département Informatique et télécommunications.**



## **Abstract :**

Arguably, biology has become an information science. We are facing a data deluge, yet all these data are worthless if we cannot use them (let alone reuse them). Moreover, the problem is not only sheer data accumulation, but the heterogeneous nature of data, the fact that they cover different scales (ranging from genome to proteins, cells, organisms to ecosystems) and their high level of interdependencies. Currently, the main bottleneck is not data generation nor data storage, but data analysis. There is a strong need for automatic tools able to handle data quantity and complexity, as well as their distributed nature. A significant part of the analysis process also relies on domain knowledge. However, these problems are not biology-specific. The W3C Semantic Web initiative provides some useful technologies for representing, sharing and query data annotations. This presentation will cover the characteristics of life science data and their analysis. Then we will provide a short overview of the Semantic Web. Finally, we will demonstrate how this made possible the reduction of the number of candidate metabolic networks from 2400 to 96 for the brown algae *Ectocarpus siliculosus*.

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## THÉMATIQUE(S)

Formation, Recherche - Valorisation

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