

NCBO-Galaxy: bridging the BioPortal web services and the Galaxy platform

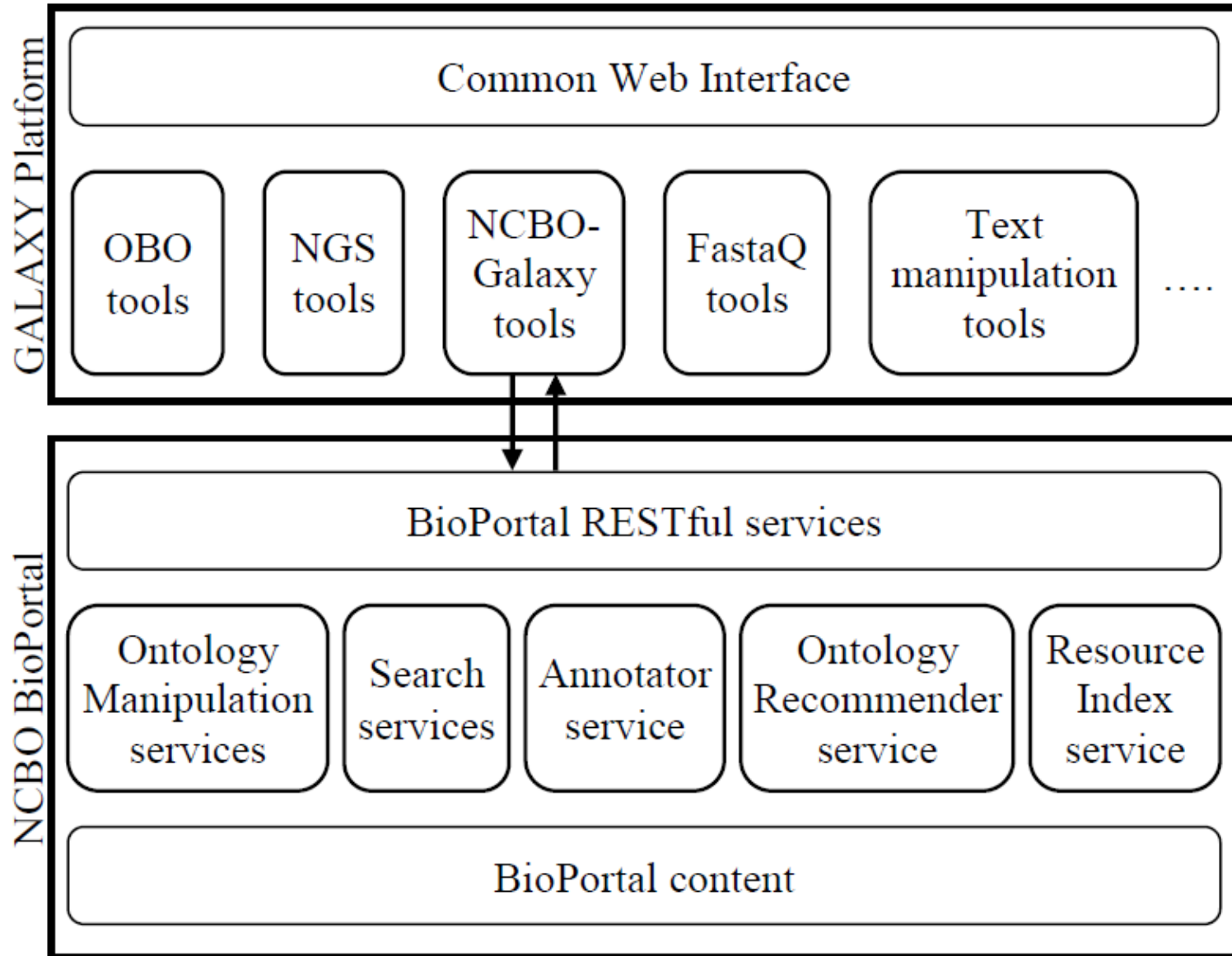


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Architecture



NCBO-Galaxy tools

- Access ontologies tools:
 - Get ontology by its identifier.
 - Extract a branch from an ontology.
 - Get a concrete view of an ontology.
- Annotator tool:
 - Annotate a text with bio-ontology terms.
- Ontology Recommender tool:
 - Recommend a bio-ontology depending on annotations of a text.
- Search tools:
 - Search for terms in bio-ontologies depending on the text provided.
 - Search for resources matched up with terms in bio-ontologies.

Software demo

- NCBO services:
 - Search for resources matched up with terms in bio-ontologies:
 - Text: “Prostate cancer”
 - Text: “Cell carcinoma”
- Text Manipulation:
 - Cut columns from a table.
- Join, subtract and Group:
 - Compare two Datasets to find common or distinct rows.

Software demo

The screenshot displays the Galaxy web interface. At the top, there is a navigation bar with the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Help, and User. Below the navigation bar, the interface is divided into three main sections:

- Tools:** A sidebar on the left containing a list of tools under the heading "NCBO services". The tools listed include "Get ontology by id", "Extract a branch from an ontology", "Get a concrete view of an ontology", "Annotates a text with bio-ontology terms", "Recommends a bio-ontology depending on annotations of a text", "Search for terms in bio-ontologies depending on the text provided", and "Search for resources matched up with terms in bio-ontologies depending on the given text".
- Workflow:** The central area shows a workflow with a table of data points. The table has two columns, each starting with a dot (•). The data rows are: PC 542578, PC 618310, PC 837679, PC 844229, DBK DB00351, DBK DB01248, DBK DB01873, UPKB 096017, UPKB 096017, UPKB 096017, UPKB P10275, UPKB P10275, UPKB P10275, UPKB P10275, UPKB P10275, UPKB P10275, UPKB P10275, PGGE PA420, PGDR PA450085, PGDR PA7000, and PGDR PA7000.
- History:** A sidebar on the right showing a list of workflow steps. The steps are numbered 21 through 25. Steps 21, 22, 23, and 24 are highlighted in green. Step 25 is "25: Compare two Datasets on data 23 and data 24". Step 24 is "24: Cut on data 21". Step 23 is "23: Cut on data 22". Step 22 is "22: Search for resources matched up with terms in bio-ontologies depending on the given text". Step 21 is "21: Search for resources matched up with terms in bio-ontologies depending on the given text". Each step includes an eye icon, a pencil icon, and a close icon (X).