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BaseSpace[®] Correlation Engine Ontology Editor Integration

Using a standardized vocabulary with external applications.

Introduction

The Ontology Editor Application within the BaseSpace Correlation Engine provides a standardized vocabulary for annotating and tagging scientific experiments. It enables searching for scientific concepts and retrieval of tagged information. Ontology Editor can be integrated with external applications or custom workflows using dedicated application programming interfaces (APIs).

Tags can be mapped to one or more of the following BaseSpace Engine ontology categories: Tissue, Biodesign, Biogroup, Biosource, Compound, Genemode, and Phenotype. More detailed documentation on data tagging is provided separately (see *Tagging Cheat Sheet for the BaseSpace Correlation Engine*).

This technical note outlines the use cases and communication interfaces for integrating the Ontology Editor with external applications.

Use Cases

Tagging Data with the Ontology Editor

Preconditions

The Ontology Editor, including the autocomplete functionality, is integrated in custom data collection applications.

Workflow

- Create and select an experiment for annotating and tagging. This action launches the data annotation form.
- Select a form box and enter a classification tag.
- The autocomplete functionality allows users to select from a list of terms that either begin with, or are synonyms of, the string as the entered classification term.
- If users are uncertain of the concept branch or term, the Ontology Editor can be launched for help with tagging.

Postconditions

The application saves classification information provided in the form boxes for the experiment of interest.

Retrieving Data Tagged with the Ontology Editor

Preconditions

The Ontology Editor, including the autocomplete functionality, is integrated in custom data collection applications.

Studies and experiments saved in the custom data collection application are annotated and tagged using the BaseSpace Engine Ontology Editor.

Workflow

- The term of interest can be entered into the custom data collection application with the help of the builtin search capabilities.
- The autocomplete functionality allows users to select from a list of terms that either begin with, or are synonyms of, the string as the entered classification term.

Postconditions

The application retrieves and displays a list of experiments tagged with the search term or its synonyms.

Integration APIs

Ontologyinfo API

The Ontologyinfo API allows the user to search and find ontology information, including descriptions, synonyms, and the type of ontology term.

Parameters

Required

q-query term

Response

An OntologyInfoObject

Example

Sample Request

/nbapi/ontologyinfo.api?/nbapi/ontologyinfo.api?q=cancer

Sample Response

"result": {

"description": "Malignant neoplastic disease",

"id": "1322843",

"synonyms": null,

"type": "disease"

}

Autocomplete API

}

The Autocomplete API returns a list of terms that start with the same string as the term of interest. It also includes synonyms of the search term.

Note: The autocomplete API uses a dedicated API key that is different from the one used for other APIs. Attempting to access the autocomplete API using the general API key will result in an error.

Parameters "type": "GENE" Required q-query term; all results will have either terms or synonyms that start with the same letter. Optional "id": 788290, nr-the number of results returned; default is 10, maximum "name": "GATAd", is 100. "synonyms": [type-a filter to return only items of the specified type; if this parameter is omitted, terms of all types will be returned. Valid types are GENE, BIOGROUP, TISSUE, DISEASE, COMPOUND, SNP, AUTHOR, BIOSOURCE, BIODESIGN, and GENEMODE. Multiple type parameters can be included; for such cases, results of all specified types will be returned. cv-command version; if omitted or set to 0, no action is taken compared to the previous version. If set to 1 (or higher),], the DISEASE type is replaced with PHENOTYPE. "type": "GENE" alttype-if true, a value is returned for type that matches the }, XML import TagType. Example types are Gene, Biogroup, Tissue, Disease, Compound, Snp, Author, Biosource, Biodesign, and Genemode. "id": 826406, "name": "GATAe", Response "synonyms": [The response is a list of Autocomplete terms. Example Sample Request /nbapi/autocomplete.api?id=gata Returns 10 results that begin with the letters "gata". Sample Response], "result": {"items": ["type": "GENE" { } "id": 10345, "name": "GATA4", "synonyms": ["GATA", "GATA binding protein 4", "Gata-4", "GATA-4", "GATA-4 transcription factor", "GATA-binding factor 4", "GATA-binding protein 4", "GATA4",

"CG5034",

"dGATA-D",

"dGATAd".

{

"Dmel_CG5034",

"DmelCG5034"

"CG10278",

"dGATA-E",

"dGATAe",

"Dmel_CG10278",

"DmelCG10278"

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