

RSAT REST API

Participants

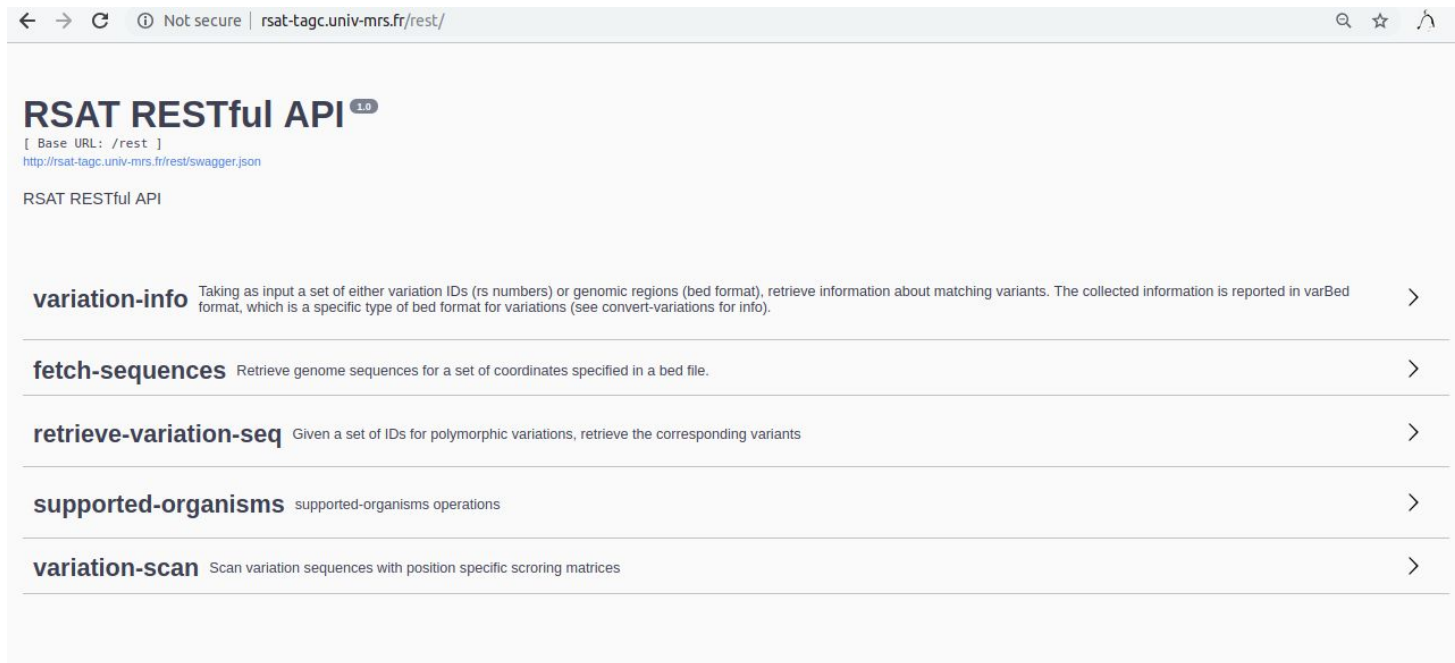
- Jacques van Helden
- Thuy Nga Thi Nguyen
- Aziz Khan
- Yvon Mbouamboua
- John Zobolas

Achievements during the hackathons

- Coverage of the initial goals
 - Add entry points required for the project "Workflow for the analysis of disease-associated regulatory variants": variation-info, retrieve-variation-seq, variation-scan
 - Develop a detailed documentation for the existing and new entry points.
 - Implement small test and demo scripts invoking these web services with various languages: python, perl, java, R.
 - Implement the functional test for workflow using R
 - Brief user guide for implementing clients and server

Illustration of the results

- Interface web for the documentation



variation-info

Taking as input a set of either variation IDs (rs numbers) or genomic regions (bed format), retrieve information about matching variants. The collected information is reported in varBed format, which is a specific type of bed format for variations (see [convert-variations](#) for info).



POST /variation-info/

Parameters

Try it out

Name	Description
species <small>★ required</small> string <i>(formData)</i>	Species name. This name must correspond to the species of the variation/bed/id file if provided <i>Default value</i> : Homo_sapiens
assembly <small>★ required</small> string <i>(formData)</i>	Assembly (e.g. GRCh37 for the assembly 37 of the Human genome) <i>Default value</i> : GRCh38
i file <i>(formData)</i>	Input file. If no input file is specified, use the input_string option
i_input_string string <i>(formData)</i>	Use this option to replace the file upload option in case there is no local file, or in the GET method. It can be a url address to the file, the result file of other tool used in workflow (piping), or the content of the input
i_input_string_type string <i>(formData)</i>	url: url address to the file. piping: result file from other tool. text: input content <i>Available values</i> : url, piping, text <i>Default value</i> : url

Responses

Response content type

application/json

2

Curl

```
curl -X POST "http://rsat-tagc.univ-mrs.fr/rest/fetch-sequences/" -H "accept: application/json" -H "Content-Type: multipart/form-data" -F "genome=mm9" -F "i_input_string_type=url" -F "u=http://rsat-tagc.univ-mrs.fr/rsat/demo_files/fetch-sequences_Schmidt_2011_mm9_CEBPA_SWENBL_R0.12_702peaks.bed" -F "header format=galaxy"
```

Request URL

<http://rsat-tagc.univ-mrs.fr/rest/fetch-sequences/>

Server response

Code

Details

200

Response body

[illegible]

What remains to be done

- Add new entry points for other tools
- Add more options for returning response
 - Already have: json and text
 - Add: yaml, xml, etc.
- Implement a nicer interface for the API documentation
- Improve the user guide