RSAT REST API

Participants

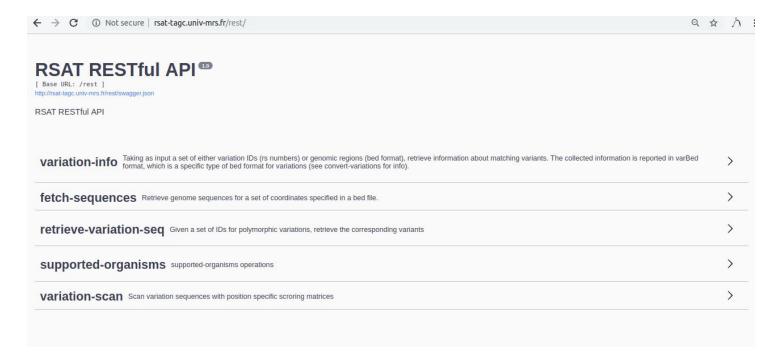
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Achievements during the hackathons

- 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).



/variation-info/ Try it out **Parameters** Name Description species * required Species name. This name must correspond to the species of the variation/bed/id file if provided string (formData) Default value: Homo sapiens assembly * required Assembly (e.g. GRCh37 for the assembly 37 of the Human genome) string (formData) Default value: GRCh38 Input file. If no input file is specified, use the input string option file (formData) i input string 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 string workflow (piping), or the content of the input (formData) i input string type url: url address to the file. piping: result file from other tool. text: input content string (formData) Available values: url, piping, text Default value : url

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_SWEMBL_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

```
"result path": "$RSAT/public html/tmp/www-data/2019/04/26/fetch sequences 2019-04-26.101951 G3Yo d/fetch-sequences 2019-04-26.102018 VjPnrg.fasta",
 "output":
">mm9 chrl 8862955 8863208 +\ncTGTCTATATGCCACCATGCTTCTTACTATGATGATAATATAAGCCTACCCAATTAAGTGTTTTCTTTTATGAGTCATTGTGTTTTCTTCACAGTAATAGAAACCCAAACACAGAAGTTGATGCCAGGGACTAGAGATATAGAGTATTGT
AGCCCAGATGCTCTCACTTGTCATGCAGTTTGTCAGGGACCAAGACCAACACCACC\n>mm9 chr1 21310405 21310630 +\nTGGGAATGGGAGTTTGCCTCATTATTTTAGGGAATTTTTAATGCAGGCATATTCATAAACTGCAATAGCTTATAT
ATCTGAAGTTGCTGGGGAAATTTTCCGATTTCAGCCCAGCAACCAGATTACAATCACCTTGGCAGAGGACTACAGCAGTTGGCAAATACACGGGTTCAAAG\n>mm9 chrl 23003563 23003832 +\ncTTTACAAATTTCAAACAAATTTTTGGGTATGACAAAGG
TCCCTGCCTTCTCCTGGACGTTGTTAACTGCTCTTTCCCCTGTCAGAGACTAAAGTCCTGCAAACCAAGTCAGGACATATTGCTTCATACAGTACAGTCCATCAGCCTTCCAATACAGACTAATAATAACAGTGCCAGGAAAAGACACTGGAAGCAGGCCGTTTC
ATCAGCAGTGTGTGGGAGAAGCCAGTTCTACTCTAACTCCAAGGGAACAACTGTGGGAACC\n>mm9 chrl 40285978 40286210 +\nAGGAACCTAAGCATCACTCTTAAGCATTACCAAAGGTCCAAAGCTTTTCAAGCCATGTCCACAGTGCC
39789 50740092 +\manaattgatcagtggtatccaatagtgggggtgatggggaaaattacataacactttgaacggtacaaacatcttgactctcagaaaatctggccaaaatcagctctctgattattgtaagcaaacagattgtgcaagcattgctagaga
GTCGAGTGAAGGTTGATGGAGGTCATTGACTTTTGAGACTAAACATTAGTTTAGAATCAGAGACCACAGGCCAAATTCCAAACCTAACCTGAAAACCTGAAACCTAACTTCTTATCTCTGAATTCCAGATTGCAAATAGAGAAAGGGTACTAA\n>mm9 chrl 51797761
51798007 +\nTCTTAAAATATTCATAACTCGAGTTGTAATATCAGAGGGACAGGATGTGTTTTTAGAAAAGGGAATTCAAAAGGGCAGCGACATGTTGCAACACAGTTACACAAATATCTCCAGAACATCCTGATTAGATGCAGCTCAGATCTGCCTGTTCCAAAGG
CCTTCTTCCCAAAATGAATTCTCAATAGAATTCAGTAACTAGCTTTTAGGTTAAGACATCTACACATATTCTCGAGCTGCATTTTAGAAGTCTATCTG\n>mm9 chrl 54609526 54609794 +\ncTTAATAGGCTAGCACTTTAAATTATCTTCTCCAAC
```

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