RESTful API

The RESTful API is a collection of 8 resources that can be accessed over HTTP. The format to retrieve data is http://hypothesis.ornl.gov/app/v1.0/ SpecificGraphReasoning?start= *start term* for applications 1 to 5, and http://hypothesis.ornl.gov/app/v1.0/ SpecificGraphReasoning?start= *start term*&end=*end term* for applications 6 to 8 (with *start term* and *end term* replaced with the actual terms). In addition, the size of the results can also be set with &size=*100*, as an example. The number of hops can be set for applications 4 and 5 (maximum = 2) and for applications 6 and 8 (maximum=7) with &hops=*5*, as an example.

You can use directly reach the resources through curl, a browser, or any programming language that can communicate through HTTP. Results are returned in JavaScript Object Notation (JSON) format.

Example of cURL command line:

App1: Specific Reasoning on Graph

http://hypothesis.ornl.gov/app/v1.0/SpecificGraphReasoning?start=Ebola_virus

```
hypothesis.ornl.gov/app/v 🗙
                  hypothesis.ornl.gov/app/v1.0/SpecificGraphReasoning?start=Ebola_virus
        G
    \rightarrow
             f
{
  "SpecificGraphReasoning": {
    "head": {
      "vars": [
        "similar",
        "count"
      ]
    },
    "results": {
      "bindings": [
        {
          "count": {
             "datatype": "http://www.w3.org/2001/XMLSchema#integer",
            "type": "typed-literal",
"value": "15"
          },
          "similar": {
            "type": "uri",
            "value": "urn:sm/Marburg_Virus_Disease"
          }
        },
```

Specific Reasoning on Graph finds terms that uniquely connect to the start term. These terms are more informative than the descriptive terms shown in **Reasoning on Whole Graph**. This search can produce novel connections and show meaningful relationships, leading to new insights.

App2: Reasoning on Whole Graph

http://hypothesis.ornl.gov/app/v1.0/WholeGraphReasoning?start=Ebola_virus

```
hypothesis.ornl.gov/app/v 🗙
        G
                 hypothesis.ornl.gov/app/v1.0/WholeGraphReasoning?start=Ebola_virus
             fi
{
  "WholeGraphReasoning": {
    "head": {
      "vars": [
        "similar",
        "count"
      ]
    },
    "results": {
      "bindings": [
        {
          "count": {
            "datatype": "http://www.w3.org/2001/XMLSchema#integer",
            "type": "typed-literal",
            "value": "1049"
          },
          "similar": {
            "type": "uri",
            "value": "urn:sm/Proteins"
          }
        },
        {
          "count": {
            "datatype": "http://www.w3.org/2001/XMLSchema#integer",
            "type": "typed-literal",
            "value": "975"
          },
          "similar": {
            "type": "uri",
            "value": "urn:sm/Antibodies"
          }
        },
```

Reasoning on Whole Graph finds terms that have many connecting links to the **Search/Start Term**. A high number of connecting links is one way of determining similarity between the terms. For the whole graph, these terms tend to be descriptive of the search term.

App3: Pattern Similarity - Whole Graph

http://hypothesis.ornl.gov/app/v1.0/PatternSimilarity?start=Ebola_virus

```
hypothesis.ornl.gov/app/v 🗙 🔪
        C
                  hypothesis.ornl.gov/app/v1.0/PatternSimilarity?start=Ebola_virus
             fi
{
  "PatternSimilarity": {
    "head": {
      "vars": [
        "similar",
        "count"
      ]
    },
    "results": {
      "bindings": [
        {
          "count": {
            "datatype": "http://www.w3.org/2001/XMLSchema#integer",
            "type": "typed-literal",
            "value": "123"
          },
          "similar": {
            "type": "uri",
            "value": "urn:sm/Virus"
          }
        },
        {
          "count": {
            "datatype": "http://www.w3.org/2001/XMLSchema#integer",
            "type": "typed-literal",
            "value": "99"
          },
          "similar": {
            "type": "uri",
             "value": "urn:sm/HIV"
          }
        },
```

Pattern Similarity – Whole Graph finds terms that have many connecting links, similar to Reasoning on Whole Graph, but also accounts for how the terms are connected (predicates). New relationships can be discovered, bringing new insights and leading to serendipitous discoveries.

App4: Browse Selected Triples

http://hypothesis.ornl.gov/app/v1.0/BrowseSelectedTriples?start=Ebola_virus

```
hypothesis.ornl.gov/app/v 🗙
                  hypothesis.ornl.gov/app/v1.0/BrowseSelectedTriples?start=Ebola_virus
        C
             fi
{
  "BrowseSelectedTriples": {
    "head": {
      "vars": [
        "p1",
        "x1",
        "avgScore"
      ]
    },
    "results": {
      "bindings": [
        {
          "avgScore": {
            "datatype": "http://www.w3.org/2001/XMLSchema#decimal",
            "type": "typed-literal",
            "value": "1.0"
          },
          "p1": {
            "type": "uri",
            "value": "urn:sm/NEG_INTERACTS_WITH"
          },
          "×1": {
            "type": "uri",
            "value": "urn:sm/Hemorrhagic_Fever__Ebola"
          }
        },
        {
          "avgScore": {
            "datatype": "http://www.w3.org/2001/XMLSchema#decimal",
            "type": "typed-literal",
"value": "0.125"
          },
"p1": {
"+vpe
            "type": "uri",
            "value": "urn:sm/Rev_NEG_PART_OF"
          },
          "x1": {
            "type": "uri",
            "value": "urn:sm/Nucleoproteins"
          }
        },
```

Browse Selected Triples shows the data as it is stored in the informative graph, and determines a score based on a measure of uniqueness of the triple. The informative graph is about 10% of the whole graph, and contains relationships that are descriptive of the terms.

App5: Browse All Triples

http://hypothesis.ornl.gov/app/v1.0/BrowseAllTriples?start=Ebola_virus

```
hypothesis.ornl.gov/app/v 🗙 🔰
                 hypothesis.ornl.gov/app/v1.0/BrowseAllTriples?start=Ebola_virus
        C
            f
{
  "BrowseAllTriples": {
    "head": {
      "vars": [
        "p1",
        "x1",
        "avgScore"
      ]
    },
    "results": {
      "bindings": [
        {
          "avgScore": {
            "datatype": "http://www.w3.org/2001/XMLSchema#decimal",
            "type": "typed-literal",
            "value": "1.0"
          },
          "p1": {
            "type": "uri",
            "value": "urn:sm/NEG_INTERACTS_WITH"
          },
          "x1": {
            "type": "uri",
            "value": "urn:sm/Hemorrhagic_Fever__Ebola"
          }
        },
```

Browse All Triples + shows the raw data as it is stored in the graph, and determines a score based on a measure of uniqueness of each triple. The results are shown sorted by score.

App6: Paths

http://hypothesis.ornl.gov/app/v1.0/Paths?start=Ebola_virus&end=GP2

```
🖊 🥌 hypothesis.ornl.gov/app/v 🗙 🔪
                  hypothesis.ornl.gov/app/v1.0/Paths?start=Ebola_virus&end=GP2
←
    \rightarrow
         C fi
{
  "Paths": {
    "head": {
      "vars": [
        "p1",
         'x1",
        "p2",
        "p3",
        "avgScore"
      ]
    },
"results": {
    "indings"
      "bindings": [
        {
          "avgScore": {
            "datatype": "http://www.w3.org/2001/XMLSchema#decimal",
            "type": "typed-literal",
            "value": "0.375617283950617283950617"
          },
           "p1": {
            "type": "uri",
            "value": "urn:sm/NEG_INTERACTS_WITH"
          },
           "p2": {
             "type": "uri",
             "value": "urn:sm/Rev_INTERACTS_WITH"
           },
           "p3": {
             "type": "uri",
             "value": "urn:sm/Rev_PART_OF"
          },
           "x1": {
             "type": "uri",
            "value": "urn:sm/Hemorrhagic_Fever__Ebola"
          },
"x2": {
"*vpe
             "type": "uri",
             "value": "urn:sm/Ebola Virus Zaire"
          }
        },
```

Paths shows the connections between two terms in the informative graph. This information is useful in discovering relationships between close as well as distant terms.

App7: Context Terms

http://hypothesis.ornl.gov/app/v1.0/ContextTerms?start=Ebola_virus&end=GP2

```
hypothesis.ornl.gov/app/v 🗙
                   hypothesis.ornl.gov/app/v1.0/ContextTerms?start=Ebola_virus&end=GP2
         G
     ->.
              f
{
  "ContextTerms": {
    "head": {
       "vars": [
         "incontext",
         "cnt"
      ]
   },
"results": {
    "indings"
      "bindings": [
         {
           "cnt": {
             "datatype": "http://www.w3.org/2001/XMLSchema#integer",
             "type": "typed-literal",
"value": "2"
           },
"incontext": {
    "'' "uri
             "type": "uri",
             "value": "urn:sm/Disease"
           }
         },
         {
           "cnt": {
             "datatype": "http://www.w3.org/2001/XMLSchema#integer",
             "type": "typed-literal",
"value": "2"
           },
           "incontext": {
             "type": "uri",
             "value": "urn:sm/Viral Proteins"
           }
         },
```

Context Terms looks for the terms that connect to both the **Start Term** and the **End Term**. The common links are an indication of a relationship, and could be used to select terms for additional path searches.

App8: Paths by Predicate Weight

http://hypothesis.ornl.gov/app/v1.0/PathsByWeight?start=Ebola_virus&end=GP2

```
hypothesis.ornl.gov/app/v ×
                   hypothesis.ornl.gov/app/v1.0/PathsByWeight?start=Ebola_virus&end=GP2
    → C<sup>2</sup>
             - ffi
←
{
  "PathsByWeight": {
    "head": {
       "vars": [
         "p1",
"x1",
         "x1",
"p2",
"x2",
         "x2",
"p3",
         "avgScore"
       ]
    },
"results": {
    "'_'_dings"
       "bindings": [
         {
           "avgScore": {
              "datatype": "http://www.w3.org/2001/XMLSchema#integer",
              "type": "typed-literal",
              "value": "207"
           },
"p1": {
              "type": "uri",
              "value": "urn:sm/NEG INTERACTS WITH"
           },
           "p2": {
              "type": "uri",
              "value": "urn:sm/Rev_INTERACTS_WITH"
          },
"p3": {
    "type": "uri",
    "ue": "urn:
              "value": "urn:sm/Rev_PART_OF"
           },
"x1": {
              "type": "uri",
              "value": "urn:sm/Hemorrhagic_Fever__Ebola"
           },
           "x2": {
              "type": "uri",
              "value": "urn:sm/Ebola_Virus__Zaire"
           }
         },
```

Paths by Predicate Weight is similar to **Paths**, except the score is based on how important the predicates have shown to be upon review. This method can produce results that are more reliable.