MUSCLE (REST)

Description

MUSCLE (MUltiple Sequence Comparison by Log-Expectation) is claimed to achieve both better average accuracy and better speed than ClustalW or T-Coffee, depending on the chosen options. Multiple alignments of protein sequences are important in many applications, including phylogenetic tree estimation, secondary structure prediction and critical residue identification.

For more information see:

- Web form: http://www.ebi.ac.uk/Tools/msa/muscle/
- Document/literal SOAP service
- MUSCLE website

Web service registry entries:

- ProgrammableWeb.com

Important

There is currently a limit of 500 sequences and 1MB of data.

We kindly ask all users of EMBL-EBI Web Services to submit tool jobs in batches of no more than 30 at a time and not to submit more until the results and processing is complete. Please ensure that a valid email address is provided. Excessive usage of a particular resource will be dealt with in accordance with EMBL-EBI's Terms of Use. Please contact us if you need further information.

Clients

Sample clients are provided for a number of programming languages. For details of how to use these clients, download the client and run the program without any arguments.

<table>
<thead>
<tr>
<th>Language</th>
<th>Download</th>
<th>Requirements</th>
</tr>
</thead>
<tbody>
<tr>
<td>Perl</td>
<td>muscle_lwp.pl</td>
<td>LWP and XML::Simple</td>
</tr>
</tbody>
</table>

For an introduction on how to run these clients and use them in workflows please see the 'EMBL-EBI, programmatically: take a REST from manual searches' webinar series.

WADL

The WADL for the MUSCLE (REST) service: http://www.ebi.ac.uk/Tools/services/rest/muscle?wadl

Resources

parameters
List parameter names.

Request

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/muscle/parameters/">http://www.ebi.ac.uk/Tools/services/rest/muscle/parameters/</a></th>
</tr>
</thead>
</table>

Response
An XML document containing a list of parameter names.

For example: http://www.ebi.ac.uk/Tools/services/rest/muscle/parameters/
**parameterdetails**
Get detailed information about a parameter.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/muscle/parameterdetails/$parameterId">http://www.ebi.ac.uk/Tools/services/rest/muscle/parameterdetails/$parameterId</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>$parameterId: the name of the parameter</td>
</tr>
</tbody>
</table>

**Response**
An XML document providing details about the parameter.
For example: http://www.ebi.ac.uk/Tools/services/rest/muscle/parameterdetails/format

**run**
Submit a job with the specified parameters.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/muscle/run/">http://www.ebi.ac.uk/Tools/services/rest/muscle/run/</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>POST</td>
<td>email User e-mail address. See Why do you need my e-mail address?</td>
</tr>
<tr>
<td>POST</td>
<td>title An optional title for the job.</td>
</tr>
<tr>
<td>POST</td>
<td>format Alignment format.</td>
</tr>
<tr>
<td>POST</td>
<td>tree Tree type.</td>
</tr>
<tr>
<td>POST</td>
<td>order Order of sequences in the alignment.</td>
</tr>
<tr>
<td>POST</td>
<td>sequence Sequences to align.</td>
</tr>
</tbody>
</table>

More detailed information about each parameter, including valid values can be obtained using the getParameterDetails(parameterId) operation.

**Response**
A plain text document containing the job identifier.

**status**
Get the status of a submitted job.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/muscle/status/$jobId">http://www.ebi.ac.uk/Tools/services/rest/muscle/status/$jobId</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>$jobId: job identifier</td>
</tr>
</tbody>
</table>

**Response**
A plain text document containing the job status.

The values for the status are:

- **RUNNING**: the job is currently being processed.
- **FINISHED**: job has finished, and the results can then be retrieved.
- **ERROR**: an error occurred attempting to get the job status.
- **FAILURE**: the job failed.
- **NOT_FOUND**: the job cannot be found.

**resulttypes**
Get available result types for a finished job.

**Request**
**Response**
An XML document detailing the available result types.

**result**
Get the job result of the specified type.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/muscle/result/$jobId/$resultType">http://www.ebi.ac.uk/Tools/services/rest/muscle/result/$jobId/$resultType</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>$jobId: job identifier</td>
</tr>
<tr>
<td></td>
<td>$resultType: type of result to retrieve. See resulttypes.</td>
</tr>
</tbody>
</table>

**Response**
A document containing the result in the requested format. The MIME type of the returned document is set according to the format.

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**MUSCLE: multiple sequence alignment with high accuracy and high throughput.**
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