MAFFT (REST)

Description
MAFFT (Multiple Alignment using Fast Fourier Transform) is a high speed multiple sequence alignment program.

For more information see:
- Web form: http://www.ebi.ac.uk/Tools/msa/mafft/
- Document/literal SOAP service
- MAFFT website

Web service registry entries:
- ProgrammableWeb.com

Important
We kindly ask all users of EMBL-EBI Web Services to submit tool jobs in batches of up to 30 at a time and to not submit more until the results and processing has completed for these. This enables users as well as the service maintainers to deal more easily with local and remote network outages as well as scheduled or unscheduled downtime.

Service provision happens on a fair-share basis. Overzealous usage of a particular resource will be dealt with in accordance to the EMBL-EBI’s Terms of Use.

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>mafft_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 MAFFT (REST) service: http://www.ebi.ac.uk/Tools/services/rest/mafft?wadl

Resources
parameters
List parameter names.

Request

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/mafft/parameters/">http://www.ebi.ac.uk/Tools/services/rest/mafft/parameters/</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>none</td>
</tr>
</tbody>
</table>

Response
An XML document containing a list of parameter names.
For example: http://www.ebi.ac.uk/Tools/services/rest/mafft/parameters/
Get detailed information about a parameter.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/mafft/parameterdetails/$parameterId">http://www.ebi.ac.uk/Tools/services/rest/mafft/parameterdetails/$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/mafft/parameterdetails/matrix.

run

Submit a job with the specified parameters.

**Request**

| URL | http://www.ebi.ac.uk/Tools/services/rest/mafft/run/ |
| POST | email | User e-mail address. See Why do you need my e-mail address? |
| | title | An optional title for the job. |
| | format | Output alignment format. |
| | matrix | Scoring matrix. |
| | gapopen | Gap creation penalty. |
| | gapext | Gap extension penalty. |
| | order | Order of sequences in alignment. |
| | nbtree | Tree rebuilding number. |
| | maxiterate | Maximum number of iterations. |
| | ffts | Perform FFTS. |
| | sequence | Input sequences. |

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**

| URL | http://www.ebi.ac.uk/Tools/services/rest/mafft/status/$jobId |
| Parameters | $jobId: job identifier |

**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**

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

**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/mafft/result/$jobId/$resultType">http://www.ebi.ac.uk/Tools/services/rest/mafft/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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Recent developments in the MAFFT multiple sequence alignment program.
Briefings in Bioinformatics 9(4):286-98
PubMed: 18372315
DOI: 10.1093/bib/bbn013