

Uzak sunucular ile haberleşmek...

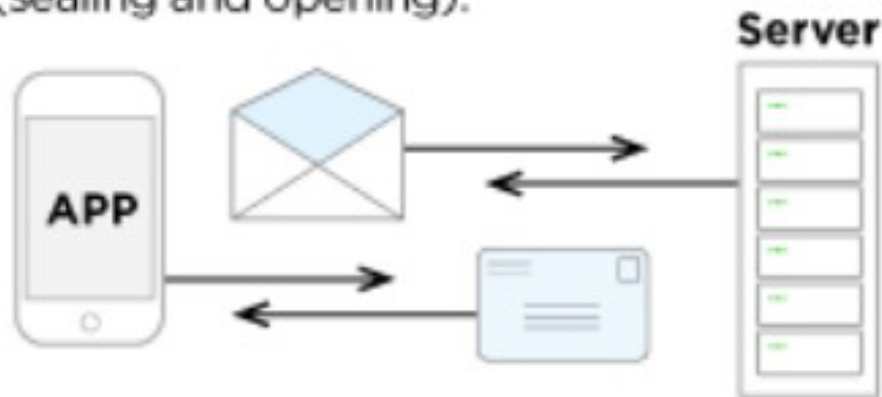
SOAP & REST



SOAP vs. REST APIs

SOAP is like using an envelope

Extra overhead, more bandwidth required, more work on both ends (sealing and opening).

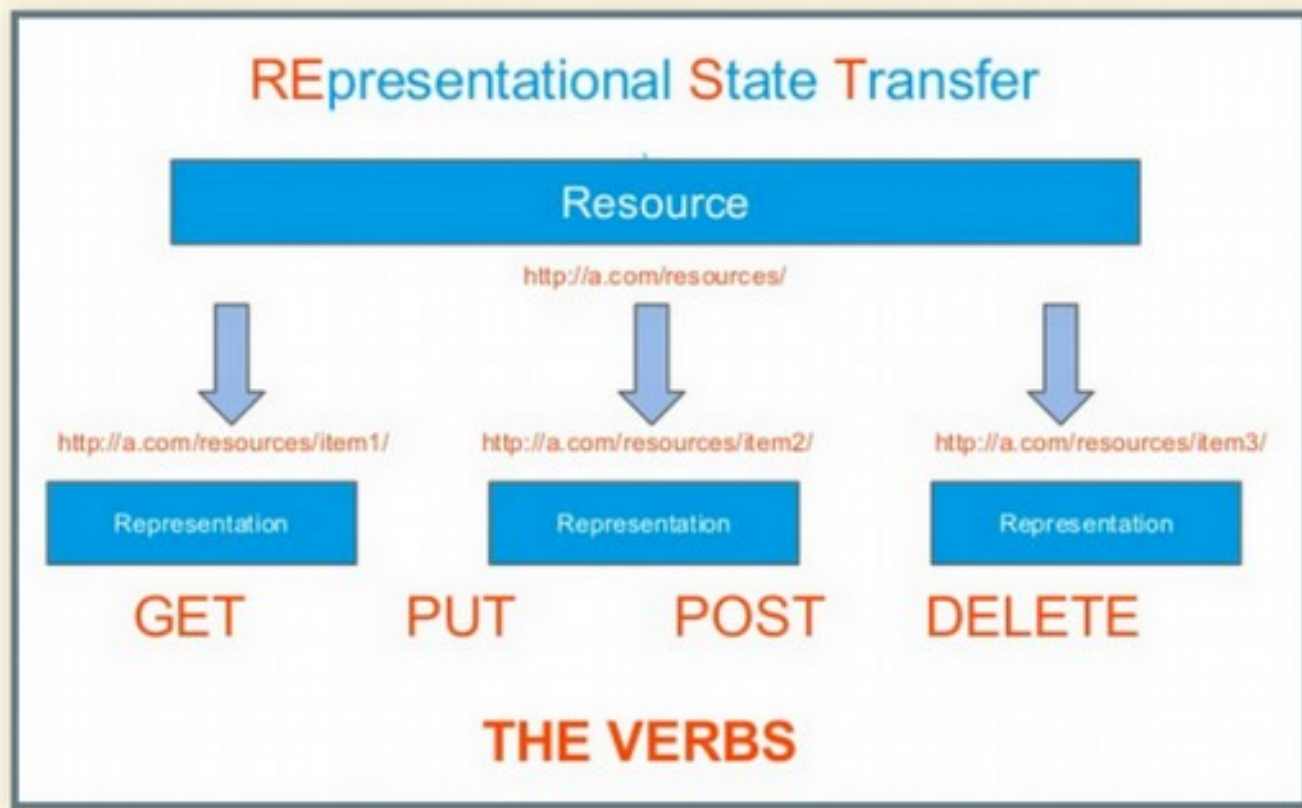


REST is like a postcard

Lighterweight, can be cached, easier to update



REST



```
from flask import Flask
from flask_restful import reqparse, abort, Api, Resource

app = Flask(__name__)
api = Api(app)

TODOOS = {
    'todo1': {'task': 'build an API'},
    'todo2': {'task': '?????'},
    'todo3': {'task': 'profit!'},
}

def abort_if_todo_doesnt_exist(todo_id):
    if todo_id not in TODOOS:
        abort(404, message="Todo {} doesn't exist".format(todo_id))

parser = reqparse.RequestParser()
parser.add_argument('task')
```

```
# Todo  
# shows a single todo item and lets you delete a todo item  
class Todo(Resource):  
    def get(self, todo_id):  
        abort_if_todo_doesnt_exist(todo_id)  
        return TODOS[todo_id]  
  
    def delete(self, todo_id):  
        abort_if_todo_doesnt_exist(todo_id)  
        del TODOS[todo_id]  
        return '', 204  
  
    def put(self, todo_id):  
        args = parser.parse_args()  
        task = {'task': args['task']}  
        TODOS[todo_id] = task  
        return task, 201
```

```
# TODOList
# shows a list of all todos, and lets you POST to add new tasks
class TodoList(Resource):
    def get(self):
        return TODOS

    def post(self):
        args = parser.parse_args()
        todo_id = int(max(TODOS.keys()).lstrip('todo')) + 1
        todo_id = 'todo%i' % todo_id
        TODOS[todo_id] = {'task': args['task']}
        return TODOS[todo_id], 201

##
## Actually setup the Api resource routing here
##
api.add_resource(TodoList, '/todos')
api.add_resource(Todo, '/todos/<todo_id>')

if __name__ == '__main__':
    app.run(debug=True)
```

Services

[Overview](#)
[A to Z](#)
[Data submission](#)
[Support](#)

The European Bioinformatics Institute (EMBL-EBI) maintains the world's most comprehensive range of freely available and up-to-date molecular data resources.

Developed in collaboration with our colleagues worldwide, our services let you share data, perform complex queries and analyse the results in different ways. You can work locally by downloading our data and software, or use our [web services](#) to access our resources programmatically.

— You can read more about our services in the journal *Nucleic Acids Research*

Tools & Data Resources



Tools

Clustal Omega



Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

Multiple sequence alignment

InterProScan



InterProScan searches sequences against InterPro's predictive protein signatures.

Protein feature detection

Sequence motif recognition

Data resources

Ensembl



Genome browser, API and database, providing access to reference genome annotation

UniProt



A comprehensive resource for protein sequence and functional annotation.

PDBe



The European resource for the collection, organisation and dissemination of 3D structural data (from PDB and EMDB) on biological macromolecules and their complexes.

Browse by type

DNA & RNA	Gene Expression	Proteins
Structures	Systems	Chemical biology
Ontologies	Literature	Cross domain

Programmatic access

EMBL-EBI web services allow you to query our large biological data resources programmatically, so that you can develop data analysis pipelines or integrate public data with your own applications. The Web Services

Data Retrieval	A list of EMBL-EBI Web Services for data retrieval.
Protein Functional Analysis (PFA)	Tools to perform protein functional analysis.
Sequence Similarity Search (SSS)	Identify potentially homologous sequences based on sequence similarity.
Multiple Sequence Alignment (MSA)	Alignment of a set of three or more, protein or nucleotide sequences.
Pairwise Sequence Alignment (PSA)	Identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid).
Phylogeny	Access to phylogenetic tree generation methods
RNA	RNA Analysis
Sequence Format Conversion	Convert between common sequence formats, or verify the formatting of a sequence.
Sequence Statistics	Analyse a sequence to determine its properties and use statistics to assign significance
Sequence Translation	Translate a coding nucleotide sequence in to a protein sequence, or back-translate from a protein sequence to a possible coding nucleotide sequence
Literature and Ontologies	Look-up ontology terms and navigate ontology relationships or access and analyse the literature

EMBL-EBI Web Services Clients

This repository provides a collection of Sample Web Service Clients to consume EBI's Job Dispatcher Web Service tools via REST and SOAP APIs.

The RESTful API interface for the Job Dispatcher Web Services is available at <https://www.ebi.ac.uk/Tools/common/tools/help/>

Sample Clients

A collection of REST sample clients for the EBI Job Dispatcher Web Services in Python, Perl and Java. These clients are generated from the service (XML) description with <https://github.com/ebi-wp/webservice-clients-generator>

- [Perl](#)
- [Python](#)
- [Java](#)

Note: A number of "older" REST and SOAP clients in a range of programming languages is now [deprecated](#) but still available for those who might be interested. In addition to Perl, Python and Java, clients are available in C#, Visual Basic .NET, Ruby and PHP, using a variety of different REST/SOAP libraries.

Running the clients

[Download the clients](#) or clone the repository:

```
git clone https://github.com/ebi-wp/webservice-clients.git
```